

FIG.1

HPP-CFC (Colony #)

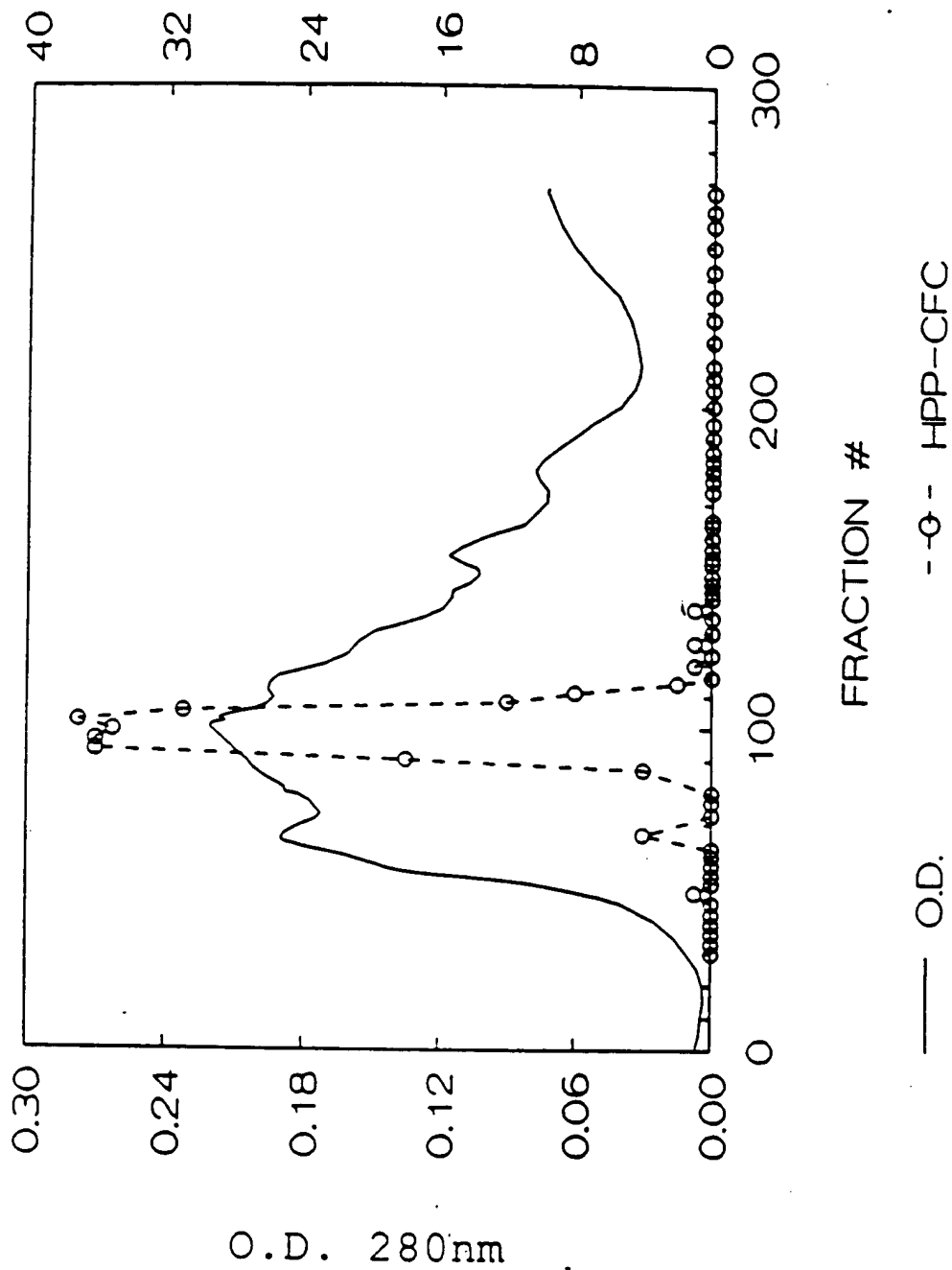
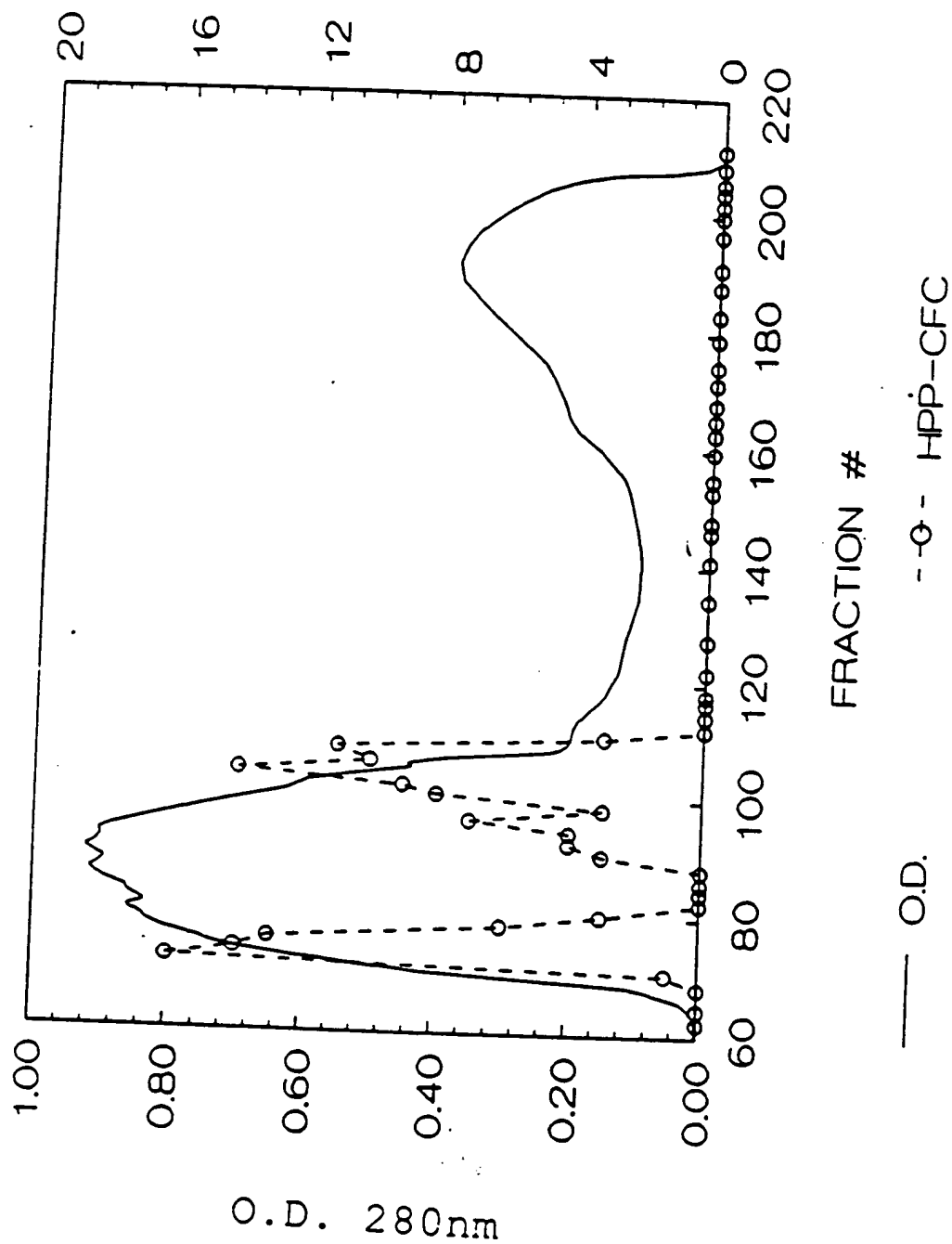


FIG.2

HPP-CFC (Colony #)



# FIG.3

MC/9 CPM ( $\times 10^{-3}$ ) OR HPP-CFC (COL. #)

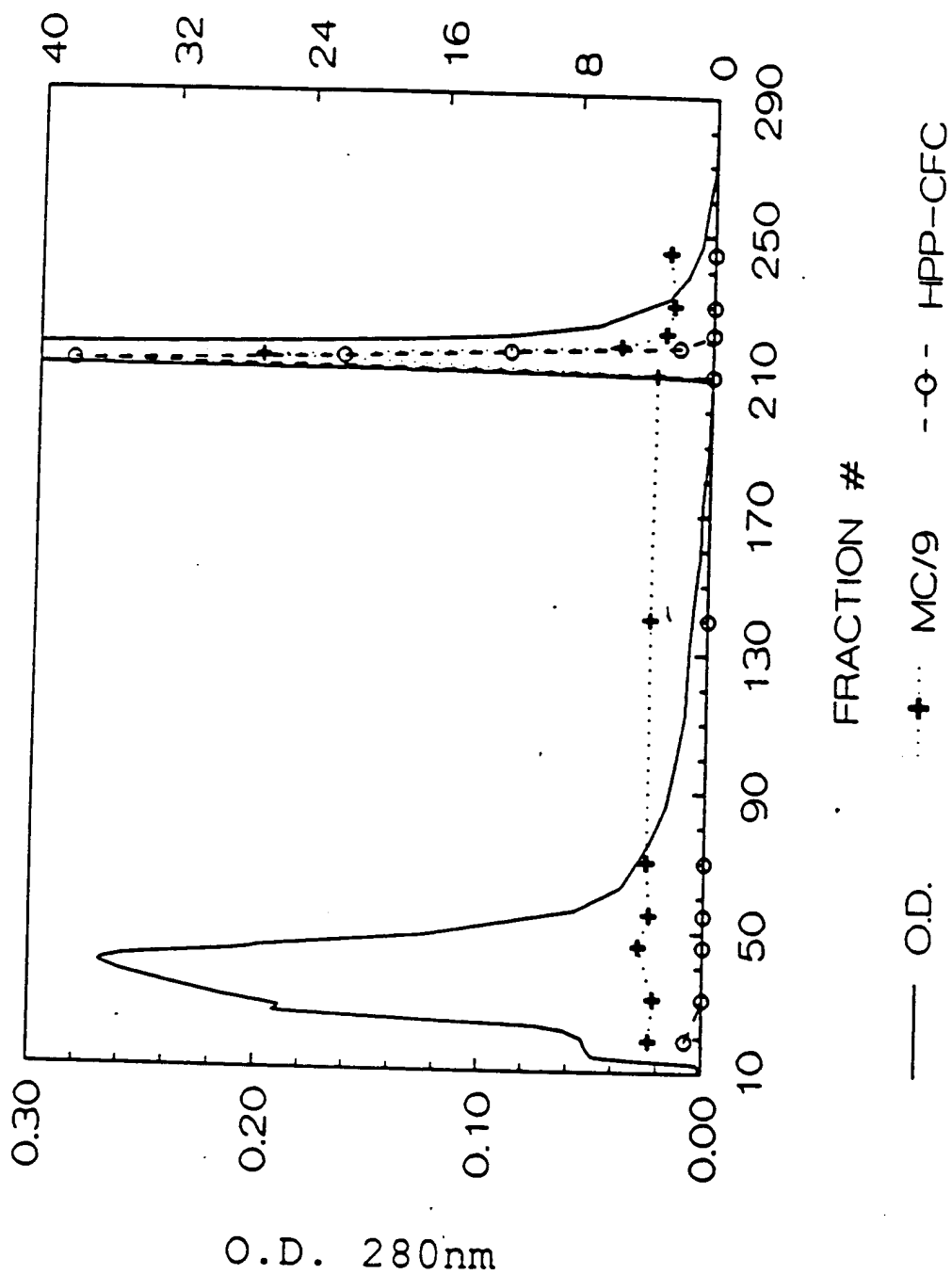


FIG. 4

MC/9 CPM ( $\times 10^{-3}$ )

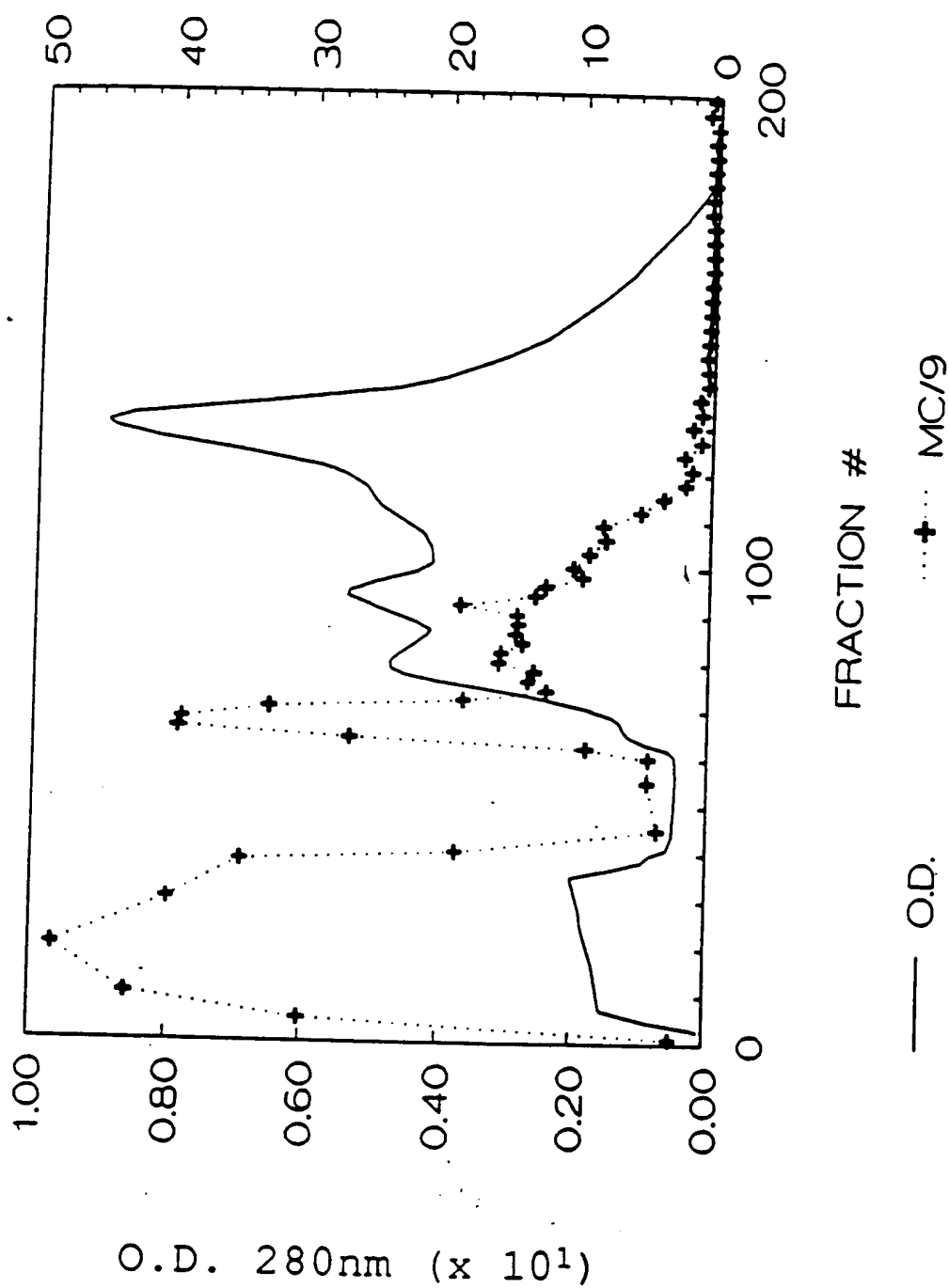


FIG.5

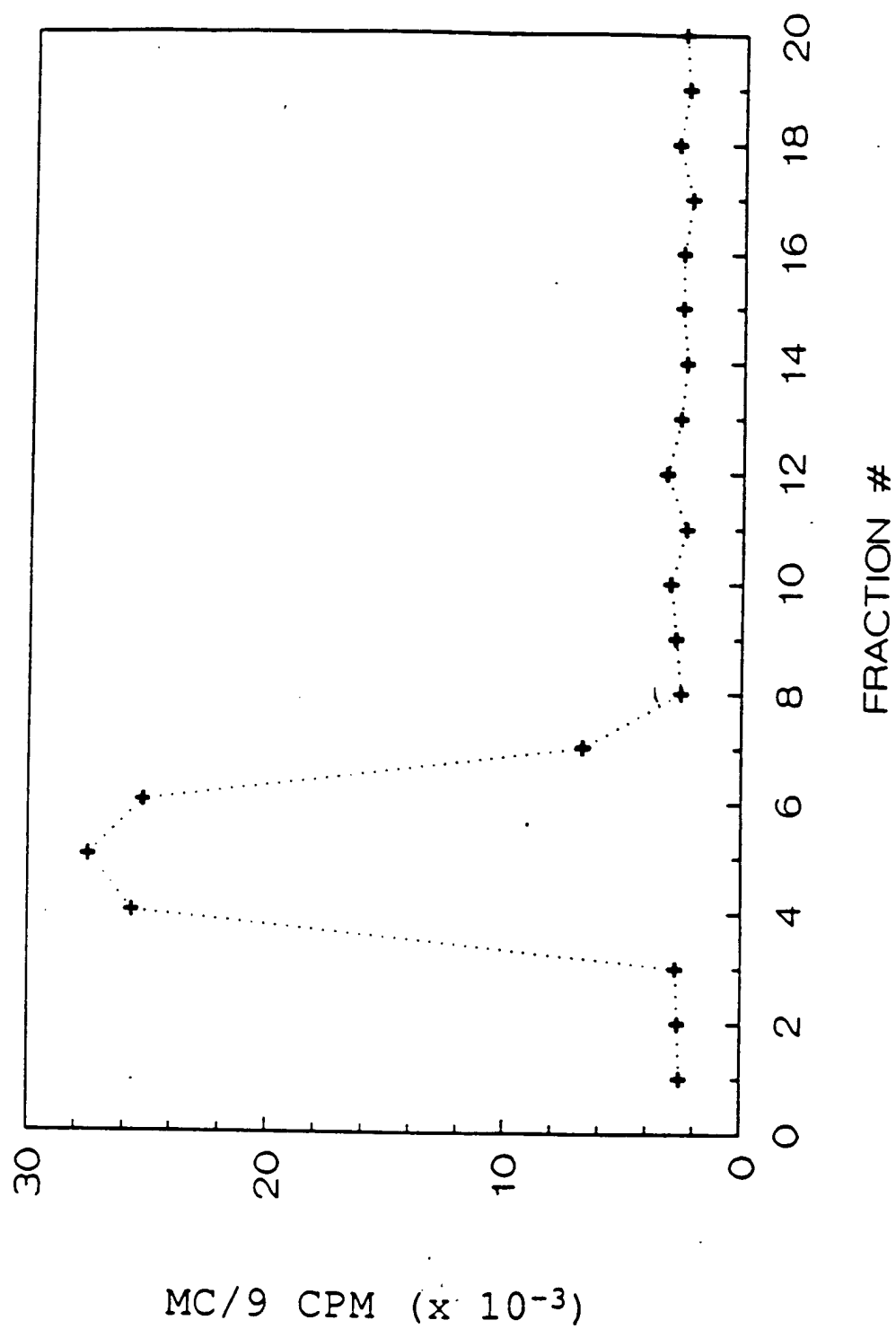
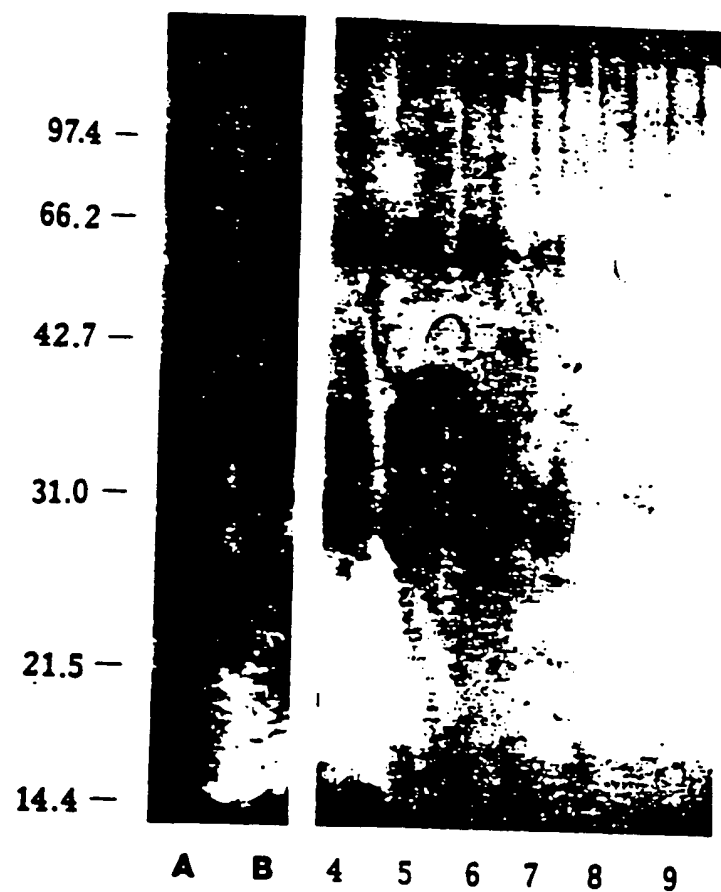


FIG. 6



# FIG.7

MC/9 CPM

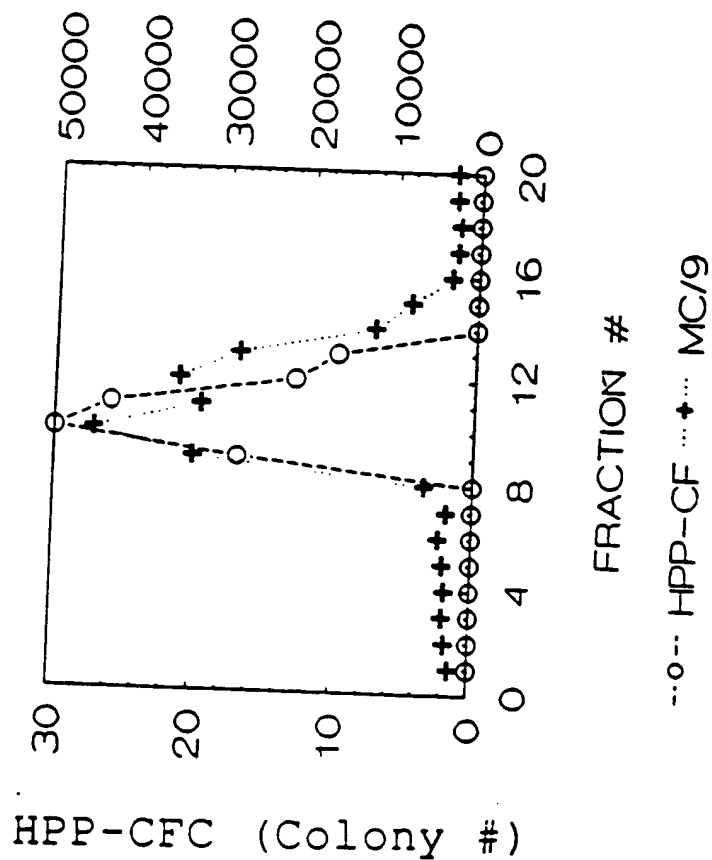


FIG. 8

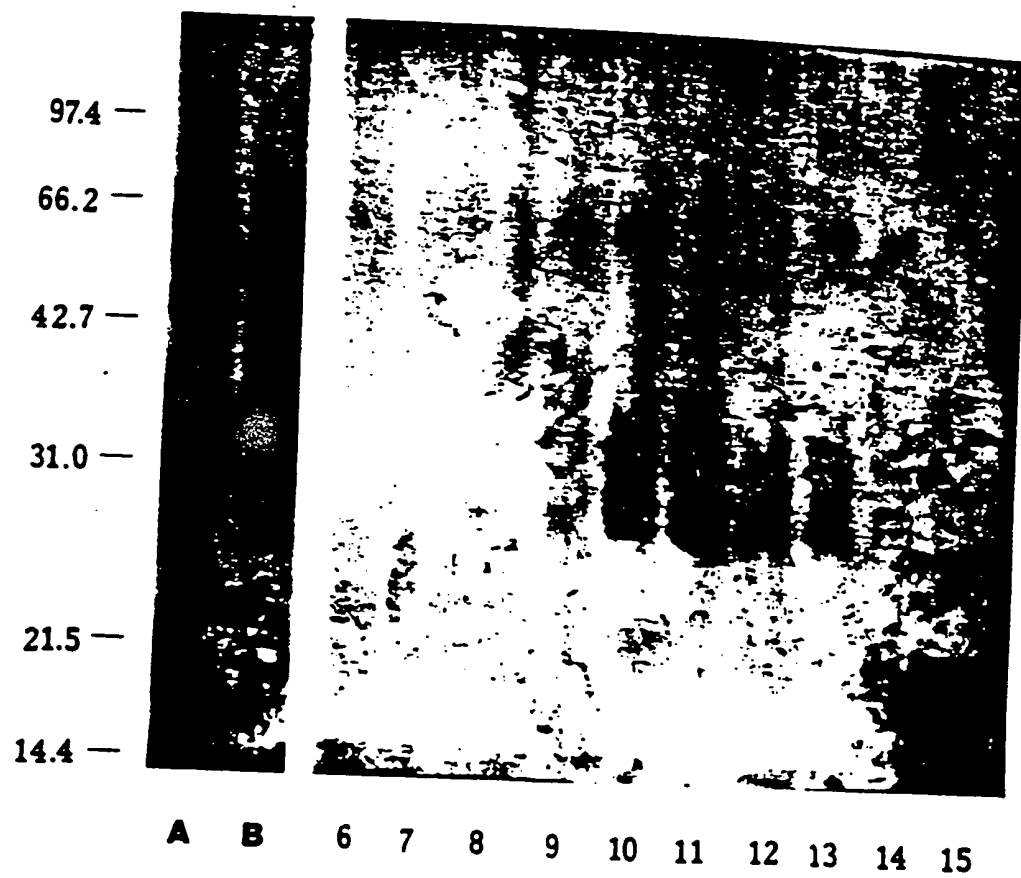




FIG.9

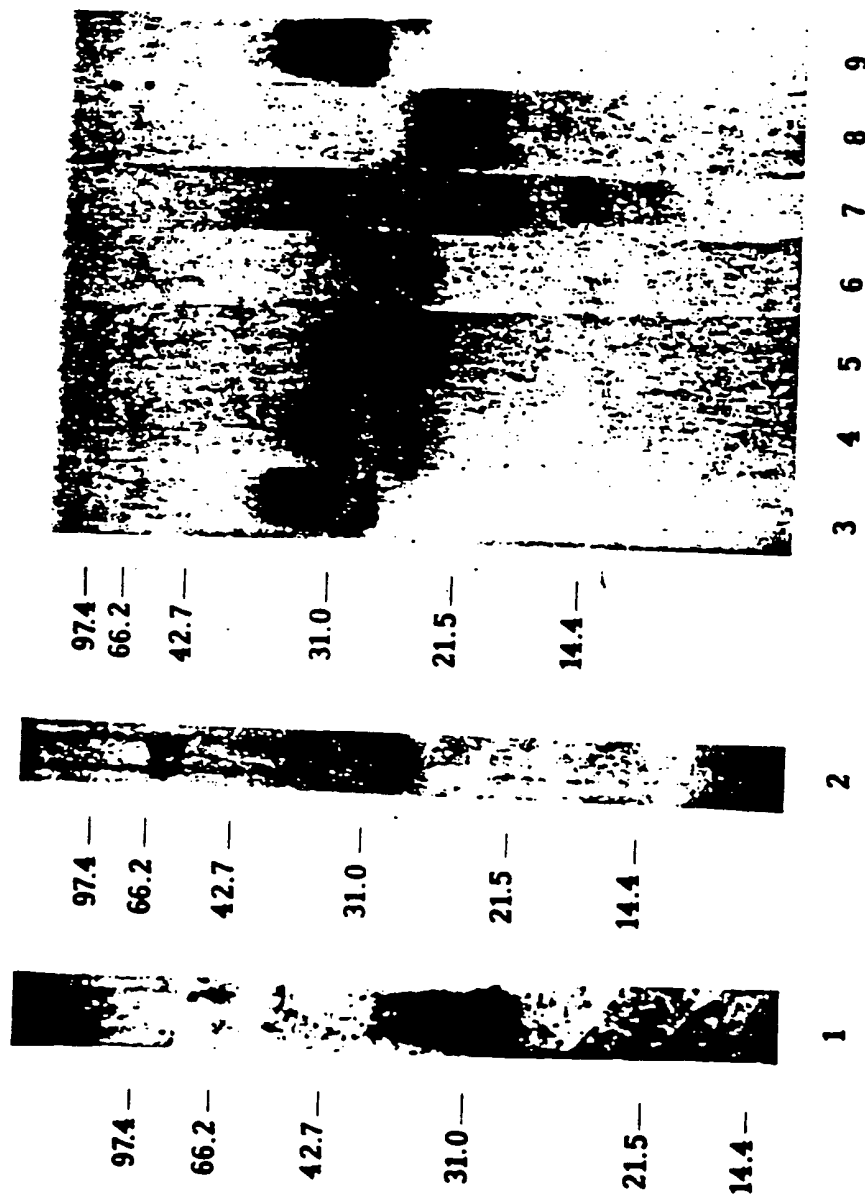
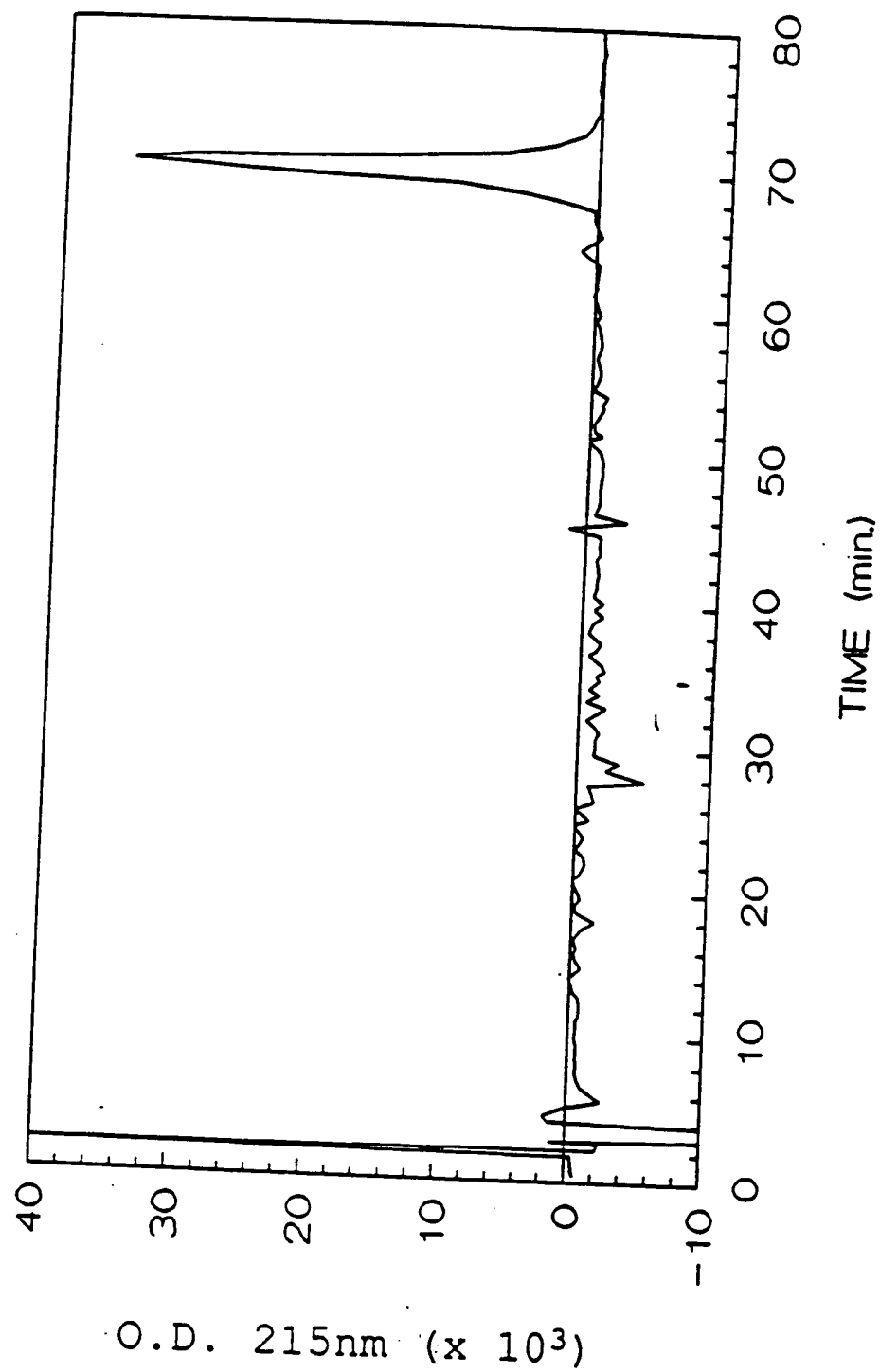


FIG.10



# FIG.11

1 10 20  
 pE E I C R N P V T D N V K D I T K L V A N L P N D  
 ----- Sequencing after  
 ----- T-5a -----  
 30 40 50  
 Y M I T L N Y V A G M D V L P S H C W L R D M V T  
 <Glu Aminopeptidase Treatment ----->  
 ----- T-5a -----  
 ----- CB-6a ----- CB-8; CB-10 -----  
 60 70  
 H L S V S L T T L L D K F S **N** I S E G L S **N** Y S I  
 ----- Sequencing after Trp Cleavage -----  
 80 90 100  
 I D K L G K I V D D L V A C M E E N A P K N V K E  
 ----->  
 ----- T-3 -----  
 ----- CB-14; CB-15; CB-16 -----  
 ----- S-1 -----  
 110 120  
 S L K K P E T R **N** F T P E E F F S I F **N** R S I D A  
 --- T-1 ----- T-4 (N109 nonglyco) -----  
 ----- T-7 (N120 glyco); T-8 (N109 nonglyco) -----  
 ----- CB-14; CB-15; CB-16 -----  
 ----- S-5 or S-6 (N109 nonglyco) -----  
 130 140 150  
 F K D F M V A S D T S D C V L S **S** **T** L G P E K D S  
 ----- T-5b -----  
 ----- CB-6B -----  
 ----- S-5 or S-6 -----  
 160  
 R V S V **T** K P F M L P P V A(A)  
 ----- T-2 -----  
 ----- CB-6B -----  
 ----- S-2 -----  
 <--- --- (Carboxypeptidase)

# FIG.12A

OLIGO	SEQUENCE	LOCATION
219-21	ACATTCTTTGGIGCATTTCTCCTCCAT G T G T T	393-368
219-22	AAAACTCCTCIGGIGTAAATTT G T T G G	447-425
219-25	GTTCNGGTTTTTT C C C	420-407
219-26	ATGGAAGAAACGCCCCCAAAACGT G G T G T	368-393
222-11	CCNAATGATTATGATAAC C C C C T	167-186
222-12	GGNGGNAACATAAANGGCTT G G T	566-585
223-6	ACCATAAAATCTTTAAACGATC G G C G G	492-470
224-24	GTATTTTCAATAGATCCATTGA	450-471
224-25	CCAACTATGTCGCC	190-202
224-27	GTAGTCAAGCTGACTGATAAG	273-253

# FIG.12A CONT.

224-28	TAACCAACAATGACTAGGCAA	235-215
225-31	TTCCAGAGTCAGTGTC	547-562
227-29	GCGAAGCTTGCCTTTCCTTATGAAGAAGA	16-35 *
227-30	GCGCCGCGGTACGGTGGTAACATGAAGGCTTTGTGA	586-561 *
228-30	GATAAATGCAAGTGATAATCC	45-65
230-25	GCGGTCGACCCGCGGAACCTTAAAGTCCATGCAACAC	705-685 *
237-19	CACCCGCGGTTATGCAACACAGGGGGTAACATAATGG	569-592 *
237-20	CACCCGCGGTTAGGCTGCAACACAGGGGGTAACATAAA	572-595 *

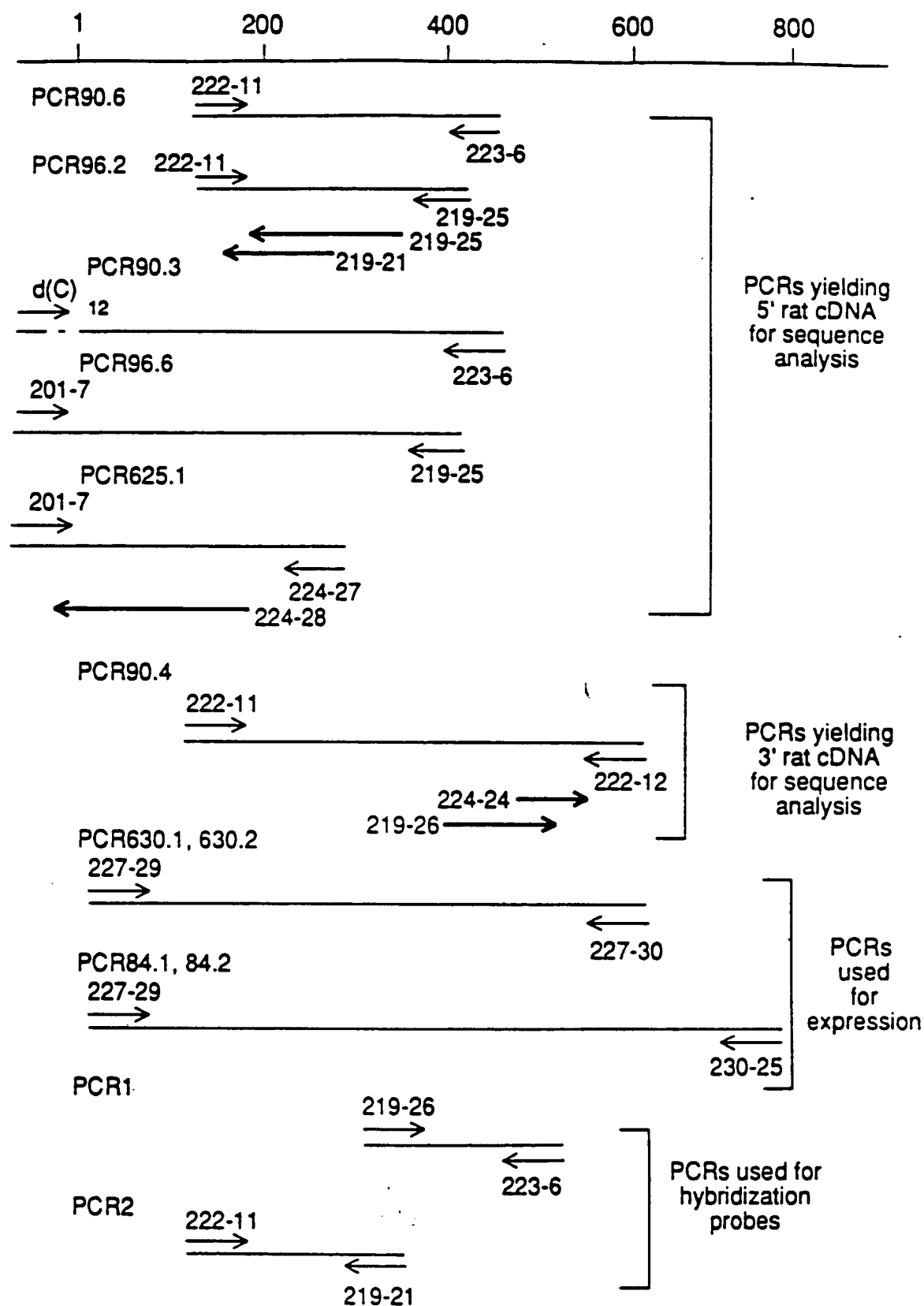
# FIG.12B

OLIGO	SEQUENCE	LOCATION
231-27	CTTAATGTTGAAGAAACC	703-686
233-13	GATGGTAGTACAATTGTCAGAC	410-431
233-14	GTCTGACAATTGTACTACCATC	431-410
235-29	CAATTTAGTGACGTCTTTTACA	302-323
235-30	TTAGATGAGTTTTCTTTCACGCAC	556-533
235-31	AAATCATTCAAGAGCCCAGAACCC	566-589
236-31	AACATCCATCCCGGGGAC	366-383
238-31	CTGGCAATATTTTAAGTCTCAAGAAGACC	
241-6	GCGCCGCGGCTCCTATAGGTGCTAATTGG	
254-9	CCTCACCACCTGTTTGTGCTGGATCGCA	153-179
262-13	GGTGTCTAGACTTGTGTCTTCTTCATAAGGA	209-190 *

## FIG.12C

OLIGO	SEQUENCE
201-7	CCCCCCCCGG T A
220-3	TTTTTTTTTTTTTTTTTTGG
220-7	TTTTTTTTTTTTTTTTTTAG
220-11	TTTTTTTTTTTTTTTTTTTCG
221-11	TTCGGCCGATCAGGCCCCCCCCC
221-12	TTCGGCCGGATAGGCCTTTTTTTTTTTTTT
228-28	GGCCGGATAGGCCTCACNNNNNT
228-29	GGCCGGATAGGCCTCAC

# FIG.13A





# FIG.13B

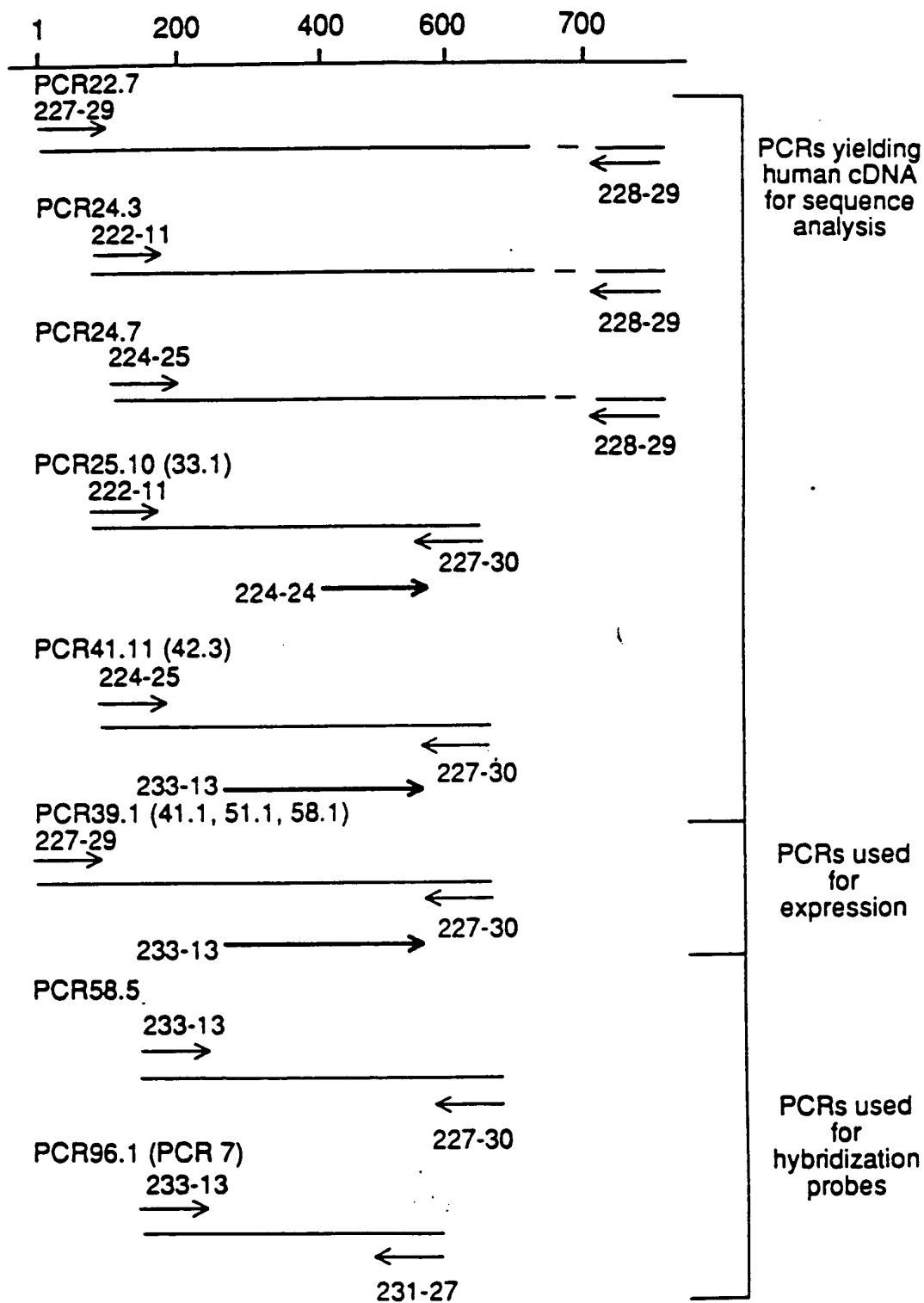
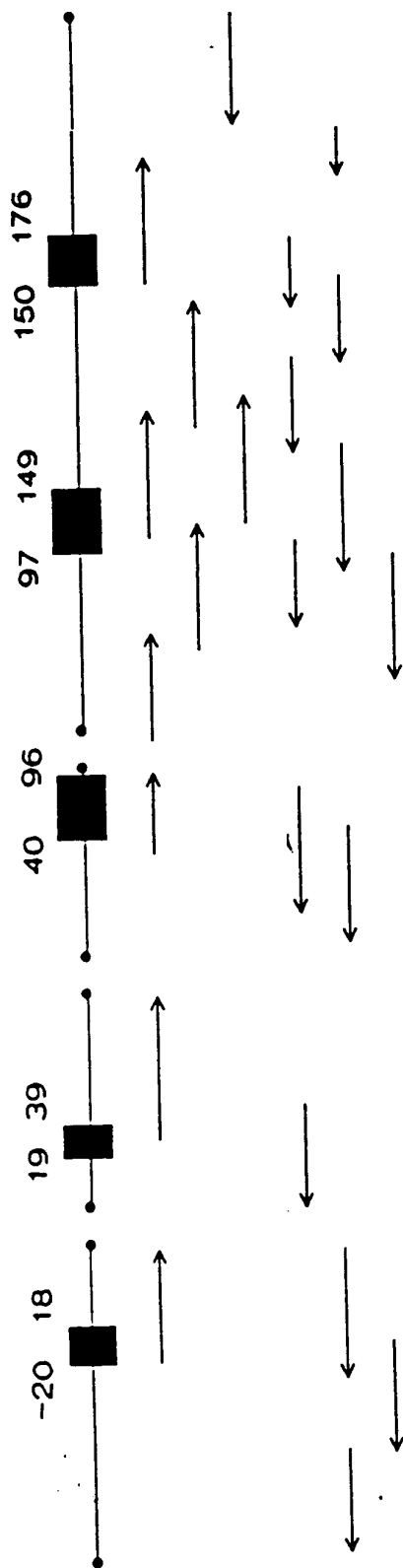


FIG.14A



# FIG.14B

AAAGTATCTTTCTATTGGCGAAGGACATGTTTTCCcATAAGTGGT	45
AAACAnACTGTCTGCACATAATAATTATCTTGCTGCCGTAAAGAT	90
TAGGTTAAATTCTGcCTTCGATCTAAAAACACACCCTTCTGTCAA	135
TCCGAGGAGCAGTGTGCTAGTCTAGAGGTCTAAATGAAGGCTCCT	180
TTCACGGTTGTATTTCTGCTCCCCAAATTGTCCACATTTAAAGG	225
AGAGTGCTTCTTTTCAGCCTTAGGCTCTGAATTTTCATGCATTCCT	270
CCATTTTCCGAGGTCCCCccCcAAGTGATAATTCTGTTACACGTTG	315
CTACAAGTTCATCCCTAATTGCCGTCAAGAACTGACTGTAGAAG	360
GCTTACCACAGACGTTGTAACCGACAGTAAAGCCATTGAAAGAGT	405
AATTCAAACAGGATGGAAGCCAGGAGTATTTTGTGGCTGTTGCTC	450
TTTTTCTTTTCAGTTTGGTGAGAGCAGCTTGAATGCTTAACATTT	495
AAGCCATCAGCTTAAAACAAAACAAAACAAAACAAAACAAAACCC	540
CGCTCTGGCATATTTGCACTTAACACATACGGTATAAGGTGTTAC	585
TGGTTTGCATAGTTCTGGATTTTTTTTTTTTTTAAAACTGATGGAC	630
	-20
	ThrTrpIleIleThrC
ACCAAGAAATGTTTCTGTTCTTTGTTTAGACTTGGATTATCACTT	675
	-10
ysIleTyrLeuGlnLeuLeuLeuPheAsnProLeuValLysThrG	
GCATTTATCTTCAACTGCTCCTATTTAATCCTCTCGTCAAAACTC	720
1	10
lnGluIleCysArgAsnProValThrAspAsnValLysAspIleT	
AGGAGATCTGCAGGAATCCTGTGACTGATAATGTAAAAGACATTA	765
	18
hrLysLeu	

# FIG.14B CONT.'

CAAAACTGGTAAGTAAAGAATGATTTTGGCATCTATAAGTCTTCC	810
CTGTGCTTGCTGACCACATAGGTTTCAGGGCACTCCCGACAGGAGT	855
TCCCAGCTTTCTAAGATAAGGAATCACTGTACGAGTCTGAAGTGC	900
TTCTTCTGGGCAAATGGGAGATGCTTAGGTCATGGAGGGTTTATC	945
TGTATAACTGGCCCTTTGCACACCAACAAAGTGACTGACTGGCTT	990
TTGCCTGTTACCTACTG	1007

Intervening sequence of unknown length

TCTCCAGTCCTGGGCATGGTATATACTTAGGCACCCAAGATTGGA	45
TTTACAACTCAAGCATTATATATTGGACAACnACGGGGTATGAGA	90
TATTAATGATATGTCAGGTTGGATGGATGAGTTTTCTCAAGAAAT	135

19

Val

TCTCTTGTATTTACTCACGTTTTTCATTTCTTGGTCTCTGTAGGTG	180
--	-----

30

AlaAsnLeuProAsnAspTyrMetIleThrLeuAsnTyrValAla	
GCGAATCTTCCAAATGACTATATGATAACCCTCAACTATGTCGCC	225

39

GlyMetAspValLeu

GGGATGGATGTTTTGGTATGTAGTCCACACACTTCTGAGTTGCCT	270
---	-----

TTTAGTAGCTAATGGGTGACCTGTGCTTATTCACATTGAAGACAT	315
---	-----

TATTTGCTCTTTGTCGTTTTTAGATGTTGACCTATAATTTTTCCT	360
---	-----

TCAAGCTGCTGCTAAGATTATCAGTGAGCATTTCAGTATGTGTTT	405
---	-----

TAAGCCTACTCATTAAAAGGAAATGGCTCATCTTAGACGTAGCAA	450
---	-----

# FIG.14B CONT.'

CCGATGTTAATTTTTCCCCAGGCATCTCTCAGAGGGACTTGAATG	495
TTAAAATCATGTTAAATTTCTCCTTGGCTATGTTATTTCTCATG	540
GCTATGTTATTCCTATTCGTATTTTCAATTTAAAGGGACGGAATATT	585
TATTGTATTTCTGAACTTTTTTCAGGCATGCATCCGGGTCTTTGAA	630
TAAAA	635

Intervening sequence of unknown length

CACTAAGACTCCTTCTAGTAATGTTTGTAATCCTGTCTGTATCGA	45
ATGTCTTTGAAAACGCAGTGACTAAGCCATAAATAATCTTCCACA	90
GAACGTCCAGTGGTTCATGAACTTTGTATGTGGGGGTGGGGCAAG	135
AATTGTCTCACTATTGGTCAAGGAAGAGAAGGTAAGGTATGCAAG	180
GGTGGTTTAAATCTTCTTCCGTGGAAGGACAAAATCATCTATCATT	225
TCCTCTGATCTCTATGCATTTGTTTGTTTTGAACTGAATCTGACT	270
TGAGCAAGAGTTGGCGTCCTGTGTTCTGAGGAACTCTTTGTCTCT	315
GCAGTCAGTGACTAAAAGTGCTGAGAGATCTGAAGAGCACTCTGA	360
ATCTGCCATATTTTTTAATAGATGCTTTGTCTTCTCTTTGAATTTT	405

40.

50

ProSerHisCysTrpLeuArgAspMetValThrHisLeu	
TTCCAGCCTAGTCATTGTTGGTTACGAGATATGGTAACACACTTA	450

60

SerValSerLeuThrThrLeuLeuAspLysPheSerAsnIleSer	
TCAGTCAGCTTGACTACTCTTCTGGACAAGTTTTCAAATATTTCT	495

70

80

GluGlyLeuSerAsnTyrSerIleIleAspLysLeuGlyLysIle	
---	--

# FIG.14B CONT.'

GAAGGCTTGAGTAATTATTCCATCATAGACAAACTTGGGAAAATA 540

90 96  
ValAspAspLeuValAlaCysMetGluGluAsnAlaProLys  
GTGGATGACCTCGTGGCATGTATGGAAGAAAATGCACCTAAGGTA 585  
ACTTGGTATTCATCAGAATTATTTTCTTATACT 619

Intervening sequence of unknown length

GAGCTCATGATGAGCAATTCACAACCACTTGTAATTCCAGCTCCA 45  
GAGGACATTATCCCCTCTTTGGATGCCATAGGAATCTGCTCTCAA 90  
ATATGTAGATAACCACTCTGCCACCTCAGCACATACATACACATA 135  
ATTAAAAAATAGAAACATTAAAGGAGTTCCAATCAATCCTTATTC 180  
TTTTCTGTATTTCAGTATGCCCAGATGTAAATTCTAGGAATATGTT 225  
TTAAAGGCTAATTCTTATTTTGTAAATAAGCAGCTTTAAATTTCTT 270  
AATTGTTTTTTTCGGGTCACCTTTATTGTCCTATTGCCACGACATTG 315  
TCCTGTCCCATTGTCTGTTATTCCTTCTGTTTTGTTTATTGTTCC 360  
CTAGTTACTTTGATCATGAGATTGACCTGTTACCCGTTGTTATTC 405  
TCTGTAGCCATTTTGAGTTGTGTCTATTAGAACAGCTGTAAATT 450  
ACTTGAATCATTGAGGACATAGTCAATAATCTATTATGCTGATCC 495  
AGTCAAGTCTATGAGTTATTTGAAAACCTAGAATCTTTGTAAATTA 540

97  
AsnValLys  
TTTGTGTTGCTTGTTTGTTTGTTTATTATTTGTCTAGAATGTAAAA 585  
100 110  
GluSerLeuLysLysProGluThrArgAsnPheThrProGluGlu

# FIG.14B CONT.'

GAATCACTGAAGAAGCCAGAACTAGAACTTTACTCCTGAAGAA	630
120	
PhePheSerIlePheAsnArgSerIleAspAlaPheLysAspPhe TTCTTTAGTATTTTCAATAGATCCATTGATGCCTTCAAGGACTTC	675
130	140
MetValAlaSerAspThrSerAspCysValLeuSerSerThrLeu ATGGTGGCATCTGACACTAGTGATTGTGTGCTCTCTTCAACATTA	720
148	
GlyProGluLysA GGTCCTGAGAAAGGTAAGGCTTTTAAGCATTCTTGTTTAAATGT	765
ACATAGAAAGCCTGAACTTCTGTAAGCCTCTACTGCTGAATCAAC	810
TAAATGTGTTGCTGTAGAAAGAACGTGTGGGTTTTTCTGATAAAA	855
ACAAAAAGCAAATATCAATGACTACCAATGATTATTATCTAGCTT	900
GAGAGATATGCCCTAAGACAGCGATTCTCGATATTTCTAAATTAA	945
AGAATTGTGTGATGGTGGCTCACATATTTTCTAACTGTGATATTT	990
GCCAGGAGAGTAGAATAATGTTATTCTTCATCCCCAGAATTCCTA	1035
AGATTTACAGTCTCATGTCTTTTCCATAAGGTTCAAACCTCTGAGA	1080
CTTGAGTTCTGAGCCTCAGCAGGTCATTCTGAATCCCCACTCTCC	1125
CCGAGCTGGGTCCCTATGGGGGAACATACTTCATTGCTTTCTTTT	1170
AAAACATGACGAGTTACCAACAGCTCCTCGCTATTATAAACATGT	1215
TCCTAAGCATGTCTGTGCATGCATAAGCCTTCACTCTACAAGAC	1260
AGTTATGGTGTATCGCTTGACAAAACCTGAGCAGCCAAGCTGAGTA	1305
TGAAATAATAATCTAGACTTGGGAGGCAGACCCAGCACCTACTGT	1350
GATATTGCACTTCGCCTTTGGGGGACTCTATGATTCAAAAGTTCA	1395

# FIG.14B CONT.

	150	
	spSerArgV	
CCATGTAACACTGACACATTATTGCTTTCTATTTAGATTCCAGAG		1440
	160	
alSerValThrLysProPheMetLeuProProValAlaAlaSerS		
TCAGTGTACAAAACCATTTATGTTACCCCCTGTTGCAGCCAGTT		1485
	170	176
erLeuArgAsnAspSerSerSerSerAsn		
CCCTTAGGAATGACAGCAGTAGCAGTAATAGTAAGTACACATATC		1530
TGATTTACTGCATGCATGGCTCCAAGTATCCTCTATAGGAGTGTT		1575
GCATGGACTTAAAGTTTATAAATCACTACTAATAATGCTGTTCTG		1620
TCACTGTTATTCCTTGTATGGGCTTCCTGACAATTAAATATCTGG		1665
TTTGTAGAATCGGATCTCCTTAGAGGTTAAGATGACCATGACAAA		1710
ATTAGGCCAATCAACTTTCTGCGAAGGTTATTTTAAATAAGGCAC		1755
GAAATTAATTGAAGGAAAAAAAAAATACAAGCAAGGCCTTATTTTG		1800
AATCATGGTAGGCTTAAATAGACTTTGTGGAGAATGTCCCTGAT		1845
CAAAGTGGAGTTTTTCAGATTTCAAGTGCATGTGCTAACTCTCCAC		1890
AATGTCAAGGCTATTTTCAGTTTTGTGTCTCCATATTTACTACTG		1935
CATGTTTGGAATTTGCTGATGCTGTTAGATTACCTAAGAATGTA		1980
TGTTGAAGAAGAATGGACTTCTTTCCCTAAAATTTCTGTCCTCTT		2025
TGcCCAAGAACCCAcGTTCCCTGGAAGACTATCTTATTTTCATGTC		2070
TGTGCAATGATCATTATAAAGATTATTGAATATACTGGGAATACT		2115
CTGGTTTCTGTTTTTACAGATTCATAATAGCTTATTCAGTCTTTA		2160
AAGAAAGTTCTCTGAAGTCCATGCTTTAGAATGTTTCTCTATCAA		2205



# FIG.14B CONT.'

AACTTGACCTGGACCTTAAATAAAGCTATATTTAGTCTTTTTATC	2250
CCTGAAAAATATATTTACAGTG TAGACATTTGATATACATCTAA	2295
GGGAAGGATGCTGCCAGAATGCTCGGGCTGGCAGTCTACAAAGTC	2340
CACTGCTCTCAGGATGGACTTCTGAAAGCGGAAATTGTGAACTGC	2385
ATGCATATAACATATCAGATCCTCGAGC	2413

# FIG.14C

-25                      -20  
 M K K T Q T W I I T C I  
 CTGGATCGCAGCGCTTCCTTATGAAGAAGACACAAACTTGGATTATCACTTGCAT    60  
  
 -10                      1  
 Y L Q L L L F N P L V K T Q E I C R N P  
 TTATCTTCAACTGCTCCTATTAACTCTCGTCAAAACTCAGGAGATCTGCAGGAATCC    120  
  
 10                      20  
 V T D N V K D I T K L V A N L P N D Y M  
 TGTGACTGATAATGTAAAGACATTACAAACTGGTGGCGAATCTTCCAAATGACTATAT    180  
  
 30                      40  
 I T L N Y V A G M D V L P S H C W L R D  
 GATAACCCCTCAACTATGTGCGCGGGATGGATGTTTGGCCTAGTCATTGTTGGTTACGAGA    240  
  
 50                      60  
 M V T H L S V S L T T L L D K F S N I S  
 TATGGTAACACACTTATCAGTCAGCTTGACTACTCTTCTGGACAAGTTTCAAATATTC    300  
  
 70                      80  
 E G L S N Y S I I D K L G K I V D D L V  
 TGAAGGCTTGAGTAATTATCCATCATAGACAAACTTGGGAAAATAGTGGATGACCTCGT    360  
  
 90                      100  
 A C M E E N A P K N V K E S L K K P E T  
 GGCAATGTATGGAAGAAATGCACCTAAGAATGTAAAGAATCACTGAAGAAGCCAGAAAC    420  
  
 110                      120  
 R N F T P E E F S I F N R S I D A F K  
 TAGAACTTTACTCCTGAAGAATTCTTTAGTATTTTCAATAGATCCATTGATGCCCTTCAA    480

# FIG.14C CONT'

```

130      D F M V A S D T S D C V L S S T L G P E
      GGACTTCATGGTGGCATCTGACACTAGTGTGTGCTCTCTTCAACATTAGGTCCTGA      540

150      K D S R V S V T K P F M L P P V A A S S
      GAAAGATTCAGAGTCAGTGTCACAAAACCATTATGTGTACCCCTGTTGCAGCCAGTTC      600

170      L R N D S S S S N R K A A K S P E D P G
      CCTTAGGAATGACAGCAGTAGCAGTAATAGGAAAGCCGCAAGTCCCCCTGAAGACCCAGG      660

190      L Q W T A M A L P A L I S L V I G F A F
      CCTACAATGGACAGCAATGGCACTGCCGGCTCTCATTTGCTTGTAAATGGCTTTGCTTT      720

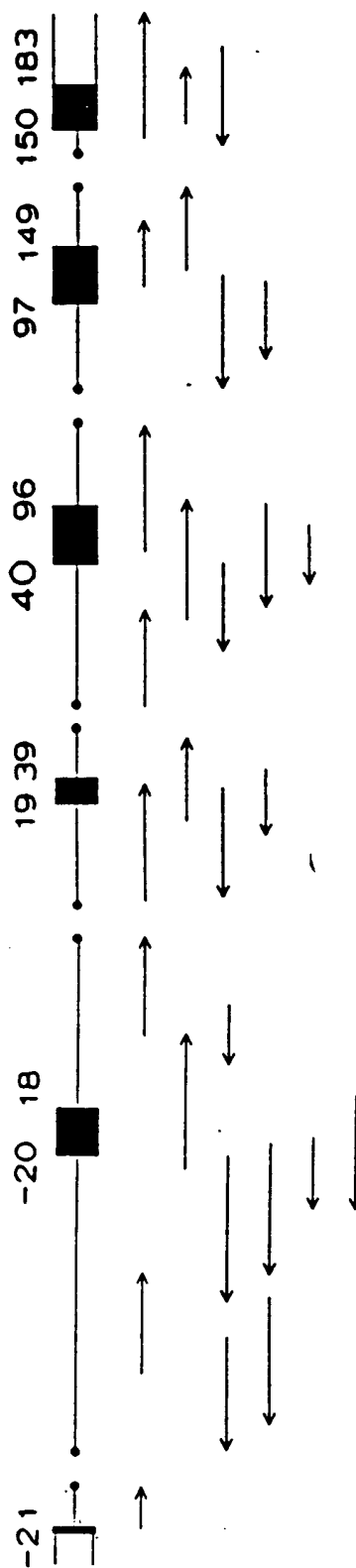
210      G A L Y W K K K Q S S L T R A V E N I Q
      TGGAGCCTTATACTGGAAGAAGAAACAGTCAAGTCTTACAAGGGCAGTTGAAAATATACA      780

230      I N E E D N E I S M L Q Q K E R E F Q E
      GATTAATGAAGAGGATAATGAGATAAGTATGTTGCAACAGAAAGAGAGAGAGTTTCAAGA      840

248      V
      GGTGTAATT      849

```

FIG.15A



# FIG.15B

-21  
hrGln

CACAAGTGAGTAGGGCGCGCCCGGGAGCTCCCAGGCTCTCCAGGA	45
AAAATCGCGCCCCGGTGCCCCGGGGaAGCCGGCGCTCCCTGGGACT	90
TGCAGCTGGGGCGTGCAGGGCTGTGCCTGCCGGGTG	126

Intervening sequence of unknown length

AGATACTACAAAGATAAATCAGTTGCACAAGTTCTTGAAACTCTA	45
CAGTGTAATAAGGAAAAATAAGTCATGCATAAAAGCAACTATAAT	90
ACATAATAGAAAATGTTATTTTCAAGCCGATGTGTAGGTTATGTG	135
TGTTTCGAGAGAGAGAGAGAGAAGACAGATTACTTTCTGCTAGGGT	180
TCAAGAATGCCTTCCTGTTGGCTAAGGAAATATTTTCCTTAAGTG	225
GCTAAAAAGCTGTGTTTCAAATATTCTTTTGATGTCTCACAAAT	270
TCAGTGGAATTCTCTTAGGTCTAAAAATATACATCTCTCTCACTT	315
TAACTTGGTGTGCTATTGTAGATTATTGGATTAAAGCACTGCTCA	360
GGGATTATGCTGCTTCTTGCCAAGCAGTCTACATTTAAAGTAGAA	405
ATAAGATGTTTCTTTTGGTGCCATAAGGTATACATTTTATGCATT	450
CTCTAGTTTTTTAGAAGATACCCTAAGGGCTAAGTCTTTAACATGC	495
TGCTACAAGTTTATTCTTAATTGCCATTGGGAAATTGGCTGAAGA	540
AAGTTTTTTAACAAAAGTTAACAATATTGTCATTGAGAGAATAATT	585
CAAAATGGATTTTAACTAAAAGCTTTTAAAACTTTGGTGAGCAT	630
AGCTTGAATGCGTAATATTTAATTGCATTTAAGCCAATAACATAT	675

# FIG.15B CONT.'

ATTAGACTGGTCTTTTTGTGCATCAAGGCATTAGATGTTAAAAGT	720
TTGAATGATTACAGATCTTAACTGATGATCACCAAGCAATTTTTC	765
<div>-20</div> <div>ThrTrpIleLeuThrCysIleTyrLeuGlnLe</div> <div>-10</div>	
TGTTTTCATTTAGACTTGGATTCTCACTTGCATTTATCTTCAGCT	810
<div>1</div> <div>uLeuLeuPheAsnProLeuValLysThrGluGlyIleCysArgAs</div> <div>GCTCCTATTTAATCCTCTCGTCAAACTGAAGGGATCTGCAGGAA</div>	855
<div>10</div> <div>nArgValThrAsnAsnValLysAspValThrLysLeu</div> <div>18</div>	
TCGTGTGACTAATAATGTAAAAGACGTCCTAAATTGGTAAGTAA	900
GGAATGCTTTACCGTGCTGTGTAAAAAAGAGCTGTGGCTCTTTTT	945
CCTGTGCTTGTTGATAAAAGATTTAGATTTTTCTTGCCCCAAAGT	990
AATGTTTTCTTAAAGTGGGGAAAGTAATCACTGGGTTACAATAAA	1035
GGGTTTATAGAAAGCAGGTAGTGAGATATTTAGGGTCATGGATAA	1080
TTTGTTGGTAAAACTGGCTAGTTGCACACCACTGCTGTGACTGCT	1125
TCTTTGCTGGTCTTCTCCCCATCCTTCATAGGCAGTGAAGGACCT	1170
TGGAGAGTTCGCTGTGTGCTGATGGGCTTGCCCCAGCTTGTTCCC	1215
CATAATCTCTCCAGTGGGTTTCCCAGCATGTTCTATTCCCCTTCA	1260
CATGTCTTCTACTCTTCTTTAAAAAGCCTAACGAAAGGAAATCT	1305
GAAATGGCTATTCTCCCAATTCAATCAGCAGGAAGACCCTGTCAC	1350
ATGTCAGTGGGTGTTTGCTCCTTCAGGGAACATAGAGAGGTGATT	1395
CATTGCCACATGTTGAAGGGACTCATCTCCCTGGTTTGTCACAT	1440
TGAACTCTTCCCTCAGCGAAAGCATTTGCATTGCTTCCC	1479

# FIG.15B CONT.'

Intervening sequence of unknown length

GAATTCCAAGATCACAGGTGGAAGCTGAAATTCAGATCATGTTTC	45
CAAACTCAGTAGGTTATACCTAGCCAGGCATAACTGAATTTGGA	90
GTCTAAAAGATCTGTATTATCACTTTTTTATTTTGAAGGATGCCT	135
TTTGATTACAGAGGGAAATCAAGGATTAAAAATCAATATACATGT	180
AAATATTGAAATTCATTGGTAACTTTAAAAAGCACACAGTTTTG	225
TGTGCTTTTCTCCAAAGCACTACAAATATGATTAATTGATGTATA	270
	19
	ValAlaA
AGAATTTTCTTATGGAATTTTTTTTTTTGTCTCTGTAGGTGGCAA	315
	30
snLeuProLysAspTyrMetIleThrLeuLysTyrValProGlyM	
ATCTTCCAAAAGACTACATGATAACCCTCAAATATGTCCCCGGGA	360
	39
etAspValLeu	
TGGATGTTTTGGTATGTAACTACATTTCTGAGTTTCATTTTAGT	405
AGCTCATAGAAGAAATGGGATCATTATGAGATAGTACACTA	450
GCTGCTATTTAGGAGCTTGCTTATTGTCAGGATTTGAAGAATTTA	495
TCTTTGGAATTTGACTTGCAGGCTTTTTTTTCCCCCTCTT	535

Intervening sequence of unknown length

CCTGTTACAAGAGTCCCTCCTCCTATTAGAATAGTCCCTCCTCCT	45
CCTGTCACACTAGTCCCTTCTCTTCCTGTTACAATAACCCCTGTC	90

# FIG.15B CONT.'

CTCCTATTACAACATTTTAAGTAATGTAATATTAATTTTAAAAAT	135
CTGGCCAGGCACGGTGGTTCATGCTTGTAATCCCAGCACATTGGG	180
AAGCTGAGACGGGTGGATCATTTGAGGTCAGGAAGTTTGAGACAG	225
CCTGGCCAACATGGTGAACTTCCTCTCTACTAAAAATAAAAAAG	270
TAGCCAGGCATGGTGGCAGGCACTTGTAATCTGAGCTACTCGAGA	315
GGCTGAGGCAGGAGAATCACTTGAGTAACTAAAACGATAGCTTTG	360
AAGAGTACTCCGAGTTTTATGGCACTTACTTATTAAAATAGCTGT	405
40	
ProSerHisCysTrpIleS	
TTTGTCTCTTTTTTCATATCTTGCAGCCAAGTCATTGTTGGATAA	450
50	
60	
erGluMetValValGlnLeuSerAspSerLeuThrAspLeuLeuA	
GCGAGATGGTAGTACAATTGTCAGACAGCTTGACTGATCTTCTGG	495
70	
spLysPheSerAsnIleSerGluGlyLeuSerAsnTyrSerIleI	
ACAAGTTTTCAAATATTTCTGAAGGCTTGAGTAATTATTCCATCA	540
80	
90	
leAspLysLeuValAsnIleValAspAspLeuValGluCysValL	
TAGACAAACTTGTGAATATAGTGGATGACCTTGTGGAGTGCGTGA	585
96	
ysGluAsnSerSerLys	
AAGAAAACCTCATCTAAGGTAACCTTGTGTTTCATTGGGATTATTTT	630
TCATTACGCTTCTCTAAAAACCCATGCTTCTTGGTGCTGTTGGGG	675
AAAATGAGGCACCTTTATTTATGATATTTTGATTGTATAAACTTC	720
AAATTTAAAAATCTTGTTCAGATGAGCAAAGAAAACAAGTATTTG	765
CAGTTATACTGCAATACTGAAGTGCACATTC	796



# FIG.15B CONT.'

Intervening sequence of unknown length

TTGTGTTCACTGCCCCAGATTCAACTTGTGATCCCACTGGGATCA	45
CTACCCTGCATTACCAATCTGAATTACATACGTAAACAGCCAT	90
CTAAAAGTGCTAGTTGTAAGAGTCTAAATACTTGAATCTTTGAGA	135
GACATATTTATAGTCCATTATCTTCACCTCAGTTAAGTCTGAAGA	180
97	
CTATTTGAAAAATGTAATCCTATTTTTTCTTCTAGGATCTAAAAA	225
110	
ysSerPheLysSerProGluProArgLeuPheThrProGluGluP	
AATCATTCAAGAGCCCAGAACCCAGGCTCTTTACTCCTGAAGAAT	270
120	
hePheArgIlePheAsnArgSerIleAspAlaPheLysAspPheV	130
TCTTTAGAATTTTAAATAGATCCATTGATGCCTTCAAGGACTTTG	315
140	
alValAlaSerGluThrSerAspCysValValSerSerThrLeuS	
TAGTGGCATCTGAACTAGTGATTGTGTGGTTTCTTCAACATTAA	360
148	
erProGluLysA	
GTCCTGAGAAAGGTAAGACATGTAAGCATTTCCAGTTCAAATGTA	405
AACAACAAACTTAAATCTTCCCTATGTAGTAAGAATCTACCTCTG	450
TGTTAAGCTGTAGCAAGATACATGCATGTACGTCTAATAAAAAAG	495
CAGATATCAATAGCACAGAAGAAA	519

Intervening sequence of unknown length

# FIG.15B CONT.'

CTCTATAACTCATACAAATCACCATATAACACTGACACATTATTG	45
<div style="display: flex; justify-content: space-between; margin: 0;"> <span>150</span> <span>160</span> </div> <div style="display: flex; justify-content: space-between; margin: 0;"> <span>spSerArgValSerValThrLysProPheMetL</span> </div>	
CTTTCTATTTAGATTCCAGAGTCAGTGTCACAAAACCATTTATGT	90
<div style="display: flex; justify-content: space-between; margin: 0;"> <span>170</span> </div>	
euProProValAlaAlaSerSerLeuArgAsnAspSerSerSerS	
TACCCCTGTTGCAGCCAGCTCCCTTAGGAATGACAGCAGTAGCA	135
<div style="display: flex; justify-content: space-between; margin: 0;"> <span>176</span> </div>	
erAsnA	
GTAATAGTAAGTACATATATCTGATTTAATGCATGCATGGCTCCA	180
ATTAGCACCTATAGGAGTATTGCATGGGCTTTCAAGGAACTTCT	225
ACATTTATTATTATTGATACTGTTCTGTTACTGTTATTCCTTTTA	270
TGGTCTTCTTGAGACTTAAGTTTGTAGAATTAAATTTCCCTAGAG	315
CTGGAGATAATGTTTAGAGAATTAGGCCAATAAATTT	352

-25	M K K T Q T W I L T C I Y L Q	
	AAGCTTGCCCTTTCCTATGAAGAAGACACAACACTTGGATTCTCACTTGCATTATCTCAG	61
-10	1	
	L L L F N P L V K T E G I C R N R V T N	10
	CTGCTCCTATTAAATCCTCTCGTCAAACACTGAAGGGATCTGCAGGAATCGGTGACTAAT	121
	20	
	N V K D V T K L V A N L P K D Y M I T L	30
	AATGTAAAAGACGCTCACTAAATTTGGTGGCAAATCTTCCAAGAACTACATGATAACCCTC	181
	40	
	K Y V P G M D V L P S H C W I S E M V V	50
	AAATATGTCCCCGGGATGGATGTTTTGCCAAGTCATGTTGGATAAGCGAGATGGTAGTA	241
	60	
	Q L S D S L T D L L D K F S N I S E G L	70
	CAATTGTCAGACAGCTTGACTGATCTTCTGGACAAGTTTCAAATATTTCTGAAGGCTTG	301
	80	
	S N Y S I I D K L V N I V D D L V E C V	90
	AGTAATTATTCATCATAGACAAACTTGTGAATATAGTGGATGACCTTGTGGAGTGCGTG	361
	100	
	K E N S S K D L K K S F K S P E P R L F	110
	AAAGAAACTCATCTAAGGATCTAAAAAATCATCAAGAGCCCCAGAACCCAGGCTCTTT	421

# FIG.15C cont.

T P E E F F R I F N R S I D A F K D F V 130  
 ACTCCTGAAGAATTCTTTAGAATTTTAAATAGATCCATTGATGCCCTTCAAGGACTTTGTA 481

V A S E T S D C V V S S T L S P E K D S 150  
 GTGGCATCTGAAACTAGTGATGTGTGGTTTCTTCAACATTAAGTCCCTGAGAAAGATTCC 541

R V S V T K P F M L P P V A A S S L R N 170  
 AGAGTCAGTGTCAACAAACCATTATGTACCCCTGTGTCAGCCAGCTCCCTTAGGAAT 601

D S S S N S K Y I Y L I 183  
 GACAGCAGTAGCAGTAATAGTAAGTACATATATCTGATTTAATGCATGGCTCCAAT 661

TAGCACCTATAGGAGTATTGCATGGGCTTTCAAGGAAACTTCTACATTATTATTATGA 721

TACTGTTCTGTACTGTTATTCCCTTTTATGGTCTTCTTGAGACTTAAGTTGTAGAATTA 781

AATTTCCCTAGAGCTGGAGATAATGTTTAGAGAATTAGG 820

FIG. 15D

GAGCTCCGAGCCCTCtCTGGCGcGcAGGTATTTCTGTGTnCCCCGGGGTGCAGGTGA 60  
 GCCCCAGCGGATCCGGAGGGTAAGCTGGGACTCCTCGCGAGCAGTAGCTGCAGGGTACC 120  
 AAGCTTCGCCCTCTGCGTCCCCCGCCCTTCGCGGTCTCCCGCCAGTGCAGGTCCGGGGCC 180  
 CCCAGGGGAGCGGACAAAGTTGGCCTAATCTGCCAAACTTCTGGGGCATTTACCGTGCTC 240  
 TGGCCGCCCTCCCGATTCTTCCCTCCCGGCCCTTGCCCTGCTTCTCGCCTACCCCGGGCTC 300  
 CGGAAGGAAGGAGGCGTGTCCGGAGCAGGGCGGGGAACTGTATAAAAGCGCCGGCGG 360  
 CTCAGCAGCCGGCTTCGCTCGCCGCCCTCGCGCCGAGACTAGAAGCGCTGCGGGGAAGCAGG 420  
 GACAGTGGAGAGGGCGCTGCGCTCGGGCTACCCAAATGCCGTGGACTATCTGCCCGCGCTGT 480  
 TCGTGCAATCTTGGAGCTCCAGAACAGCTAAACGGAGTCGCCACACCACCTGTTTGTGC 540

-25                      -21  
 MetLysLysThrGln

TGGATCGCCTTCCCTTATGAAGAAGACACAAAGTGAGTAGGGCGGCCCGGGA 600  
 GCTCCCAGGCTCTCCAGGAAAAATCGCGCCCGGTGCCCGGGGAAGCCGGCTCCCTGG 660  
 GACTTGCAGCTGGGGCGTGCAGGGCTGTGCCTGCCGGGTGAGACAAGAGGATGCGGGGGA 720  
 GGCCGGCGTGTGTGATCCCCGAGCCGAGCCGnnTGAGCCAGGGAGAAAAGGAGTGGGA 780  
 GTnCTGAGAGGGAGCCAGTGTCAAGTTTGGAGCCCTCAGCAGTTAAGTTTGTAGCTGTGAG 840  
 TCGGAAACCGTAAATTCCTGCTGTTGGAAAGATTGGCTTTnGCCACGGAATGTAAGTT 900  
 ATCAC 905

FIG. 15D CONT.

Intervening sequence of unknown length

AGATACTACAAAGATAAAATCAGTTGCACAAGTTCTTGAAACTCTACAGTGTAATAAGGAA	60
AAATAAGTCATGCATAAAAGCAAACTATAATAFACATAATAGAAAAATGTTATTTCAAAGCCGA	120
TGTGTAGGTTATGTGTGTTTCGAGAGAGAGAGAGAGACAGATTACTTTCTGCTAGGGT	180
TCAAGAATGCCCTTCCFTGTTGGCTAAAGGAAATATTTCTTAAGTGGCTAAAAAGCTGTGT	240
TTCAAAAATATTTCTTTTGATGTCCTCACAAATTCAGTGGAAATCTCTTAGGCTAAAAAATAT	300
ACATCTCTCTCACCTTTAACTTGGTGTGCTATTGTAGATTATTGGATTAAAGCACTGCTCA	360
GGGATTATGCTGCTTCTTGCCAAGCAGTCTACATTTAAAGTAGAAAAATAAGATGTTTCTTT	420
TGGTGCCATAAGGTATACATTTTATGCATTCTCTAGTTTTTAGAAGATACCCCTAAGGGCT	480
AAGTCTTTAACAATGCTGTACAAAGTTTATTCCTAATTGCCATTGGGAAATTGGCTGAAGA	540
AAGTTTTTAACAAGTTAACAATAATTGTCAATTGAGAGAAATAATCAAAATGGATTTTAA	600
CTAAAAGCTTTAAAAAACTTTGGTGAGCATAGCTTGAATGCGTAATATTTAATTGCATTT	660
AAGCCAATAACATATATTAGACTGGTCTTTTGTGTCATCAAGGCATTAGATGTTAAAGT	720
-20	
TTGAATGATTACAGATCTTAACTGATGATCACCAAGCAATTTTCTGTGTTTTCATTTAGAC	780
Th	
rTrpIleLeuThrCysIleTyrLeuGlnLeuLeuLeuPheAsnProLeuValLysThrG1	
TTGGATTCTCACTTGCAATTTATCTTCAGCTGCTCCTATTTAATCCTCTCGTCAAAACTGA	840

FIG. 15D cont.

1 uGlyIleCysArgAsnArgValThrAsnAsnValLysAspValThrLysLeu 18  
 AGGGATCTGCAGGAATCGTGTGACTAATAATGTAAGACGTCACATAAATTGGTAAGTAA 900  
 GGAATGCTTTACCGTGCTGTGTAAAAAGAGAGCTGTGGCTCTTTTTCCTGTGCTTGTGAT 960  
 AAAAGATTTAGATTTTCTTGCCCCAAAGTAATGTTTTCCTAAAGTGGGAAAGTAATCA 1020  
 CTGGGTTACAATAAAGGTTTATAGAAAGCAGGTAGTGAGATATTTAGGGTCATGGATAA 1080  
 TTTGTTGGTAAAACTGGCTAGTTGCACACCAGTCTGTGACTGCTTCTTTGCTGGTCTTC 1140  
 TCCCCATCCTTCATAGGCAGTGAAGGACCCTTGGAGAGTTCGCTGTGTGCTGATGGGCTTG 1200  
 CCCCAGCTTGTTCCCCATAATCTCTCCAGTGGGTTTCCCAGCATGTCTATTTCCCTTCA 1260  
 CATGTCTTCC'FACTCTTCTTTAAAAAGCCTAACGAAAGGAAATCTGAAATGGCTATTCTC 1320  
 CCAATTCAATTAAGCAGGAAGACCCCTGTACATGTGAGTGGGTGTTTGTCTCCTTCAGGGAA 1380  
 CATAGAGAGCTTATTCATTGCCCCACATGTTGAAGGGACTCATCTCCCTGGTTTGTACAT 1440  
 TGAAC'TCTTCCCTCAGCGAAAGCATTTTGCATTGCTTCCC 1479

Intervening sequence of unknown length

GAATTCCAAGATCACAGGTGGAAGGTGAAATTCAGATCATGTTTCCAAAACCTCAGTAGGT 60  
 TATACCTAGCCAGGCATAACTGAATTTGGAGTCTAAAAGATCTGTATTATCACCTTTTAA 120  
 TTTTGAAGGATGCCCTTTTGATTACAGAGGGGAAATCAAGGATTAAAAATCAATATACATGT 180

FIG. 15D CONT.

AAATATTGAAATTCATTGGTAACTTTAAAAAGCACAAACAGTTTGTGTGCTTTTCTCTCAA 240  
 AGCACTACAAATATGATTAAATTGATGTATAAGAAATTTCTTATGGAAATTTTCTTTTGTGT 300  
 19  
 ValAlaAsnLeuProLysAspTyrMetIleThrLeuLysTyrValProGlyM 30  
 CTCGTAGGTGGCAAATCTTCCAAAAGACTACATGATAACCCCTCAAAATATGTCCCCGGGA 360  
 39  
 etAspValLeu  
 TGGATGTTTGGTATGTAAACTACATTTCTGAGTTTCATTTTAGTAGCTCATAGAAGAAA 420  
 TGGGATCATTCATATGAGATAGTACACTAGCTGCTATTTAGGAGCTTGCTTATTGTCAG 480  
 GATTTGAAGAATTTATCTTTTGGAAATTGACTTGCAGGCTTTTTTCCCCCTCTT 535

Intervening sequence of unknown length

CCTGTACAAATCTCCCTCCTCCTATTACAAATAGTCCCCTCCTCCTGTCACTAGTC 60  
 CCTTCTCTCTCTGTTACAAATAACCCCTGTCTCCTCTATTACAAACATTTTAAAGTAATGTAAT 120  
 ATTAATTTTAAAAAATCTGGCCAGGCACGGTGGTTCATGCTTGTAATCCCAGCACATTGGG 180  
 AAGCTGAGACGGGTGGATCATTTGAGGTCAGGAAGTTTGAGACAGCCTGGCCAAACATGGT 240  
 GAAACTTCCTCTCTACTAAAAATAAAAAAGTAGCCAGGCATGGTGGCAGGCACCTTGTAAT 300  
 CTGAGCTACTCGAGAGGGCTGAGGCAGGAGAATCACTTGAGTAACTAAAAACGATAGCTTTG 360  
 AAGAGTACTCCGAGTTTATATGGCACTTACTTATTAATAATAGCTGTTTGTCTCTTTTTC 420



FIG. 15D CONT.

40	ProSerHisCysTrpIleSerGluMetValGlnLeuSerAspSerL	50	
	ATATCTTGCAGCCCAAGTCATTTGTTGATAAGCGAGATGTTAGTACAATTGTCAGACAGCT	480	
60	euThrAspLeuLeuAspLysPheSerAsnIleSerGluGlyLeuSerAsnTyrSerIleI	70	
	TGACTGATCTTCTGGACAAGTTTCAAATATTTCTGAAGGCTTGAGTAATTATTCCATCA	540	
80	leAspLysLeuValAsnIleValAspAspLeuValGluCysValLysGluAsnSerSerL	90	
	TAGACAAACTTGTGAATATAGTGGATGACCTTGTGGAGTCCGTGAAAGAACTCATCTA	600	
96	ys		
	AGGTAACTTTGTGTTTCATTTGGGATTATTTTTCATTACGCTTCTCTAAAACCCATGCTTC	660	
	TTGGTGCTGTTGGGGAAAATGAGGCACCTTTATTTATGATATTTTGTATTGATAAACTTC	720	
	AAATTTAAAATCTTGTTCAGATGAGCAAAAGAAACAAGTATTGTCAGTTATACTGCAAT	780	
	ACTGAAGTGCACATTC	796	
Intervening sequence of unknown length			
	TTGTGTTCACTGCCCCAGATTCAACTTGTGATCCCCTGGGATCACTACCCGTGCATTACC	60	
	AATCTGAATTACATACGTTAAACAGCCCATCTAAAAGTGCTAGTTGTAAGAGTCTAAATA	120	
	CTTGAATCTTTGAGAGACATATTTATAGTCCATTATCTTCACCTCAGTTAAGTCTGAAGA	180	
97	AspLeuLysLysSerPheLysSerP		
	CTATTTGAAAAAATGTAATCCTATTTTCTTCTTAGGATCTAAAAAAATCATTCAGAGCC	240	

110 roGluProArgLeuPheThrProGluGluPhePheArgIlePheAsnArgSerIleAspa  
 120 CAGAACCAGGCTCTTTACTCCTGAAGAATTCTTTAGAAATTTTAAATAGATCCATTGATG 300  
 130 laPheLysAspPheValValAlaSerGluThrSerAspCysValValSerSerThrLeuS  
 140 CCTTCAAGGACTTTGTAGTGGCATCTGAAACTAGTGATTGTGTGGTTTCTTCAACATTAA 360  
 148 erProGluLysA  
 GTCCGTGAGAAAGGTAAGACATGTAAGCATTTCCAGTTCAAATGTAAACAACAACTTAAA 420  
 TCTTCCCTATGTAGTAAGAATCTACCTCTGTGTAAAGCTGTAGCAAGATACATGCATGTA 480  
 CGTCTAATAAAAAAGCAGATATCAATAGCACAGAAGAACTAATGATTGTAGATTGTGTGGG 541

Intervening sequence of unknown length

CTCTATAACTCATACAAATCACCATATACACTGACACATTATTGCTTCTTATTAGATT 60  
 150 spS  
 erArgValSerValThrLysProPheMetLeuProProValAlaAlaSerSerLeuArgA  
 160 CCAGAGTCAGTGTACAAAACCATTTATGTTACCCCTGTTGCAGCCAGCTCCCTTAGGA 120  
 170 snAspSerSerSerAsna  
 ATGACAGCAGTAGCAGTAATAGTAAGTACATATATCTGATTAAATGCATGCGCTCCA 180  
 ATTAGCACCTATAGGAGTATTGCATGGGCTTTCAAGGAAACTTCTACATTATTATTATT 240  
 GATACTGTTCTGTACTGTATTCCCTTTATGGTCTTCTTGAGACTTAAGTTTGTAGAAT 300

FIG. 15D CONT.

TAAATTCCCTAGAGCTGGAGATAATGTTTAGAGAAATTAGGCCAATAAATTTCTGCTGA 360  
GGTTATTTTAAATAAGACATAAAAATTAATTTTAGAAATATGATTTATGCCCTTTTGTGAA 420  
TCATTAACATATAT 434

Intervening sequence of unknown length

ACAGAAACAGTTAAACAACCCACAGCATAAGAGAAAACCTTCTAGAATGGATATGCTGTA 60

178

TTCAATCAGTGTGTTCTTTAAATTATAGGGAAGGCCAAAAATCCCCCTGGAGACTCCAGCC 120  
rgLysAlaLysAsnProProGlyAspSerSerL

190

200

euHisTrpAlaAlaMetAlaLeuProAlaLeuPheSerLeuIleIleGlyPheAlaPheG 180  
TACACTGGGCAGCCCATGGCATTGCCAGCATTTGTTTCTCTTATAAATTGGCTTTGCTTTTG

213

lyAlaLeuTyrPhePheLys 240  
GAGCCTTATAC'TGGAAGGTAAGTGGTACCATTCCCTTTTAAAAAATATGCTATGTCTAC

ATAAATTATCATCTTTTTTTCCTCAAGAAATGATCCTTtAAGAAAAACAGTGAATCTACCT 300

TAGCTTATACTAAACAAAATTTAAATTTTATAAAGTTTCCTGTTTCTCATTTATGTCTGGA 360

GACAATCCCCTCTAGCTGATAATTCACGCTTAAGAATTAGGAACT 404

Intervening sequence of unknown length

FIG. 15D CONT.

AAAACTGTTATTGGAGTTATTGCCATAAAAGATAAAAGTGGAGTCCACTTACCTCTTAAA 60  
 214  
 TATTAGACCATTTCATTGATTATTTTACAGTATATGTCTTTCTTCTTTTCCAGAAAGAGAC 120  
 LysArgG  
 220  
 InProSerLeuThrArgAlaValGluAsnIleGlnIleAsnGluGluAspAsnGluIleS 235  
 AGCCAAAGTCTTACAAGGGCAGTTGAAAATATACAAATTAATGAAGAGGATAATGAGATAA 180  
 e  
 GGTATTTGTTTTGGCTAAATGTGTgCCCCAATCAAGCATGACATTGCCATTTCACACACTG 240  
 TGTACCTGCCCATTAATGTCTTTAAAGAAGTCCTTCACTCATGACAGTAGCTCCTAACCAGT 300  
 GAGTCCCAACTCTATCCATGTTTCTGTGATGTCTCACTCTCTCTTC 344  
 Intervening sequence of unknown length  
 GTATGTGTATATGCATATACAGAGAAAGAAATGTTTAACTACTTGGAAGACTACCTTA 60  
 AGACAAATGAAGTCTTCCCCTCTTCCCCTATAGTAATAAGAGTAGGCTCCCCCATTCAT 120  
 TTTGCAATCTTCTGCTACTATATTTACAGAAAAGCTGCCTTTTACAATGCCGAGATCATG 180  
 GTGTACCTCAGAAATCTCTGACCAAGAGCAAAATAAGCATTTTCTTATTGTTTTTCAGTA 240  
 237  
 etLeuGlnGluLysGluArgGluPheGlnGluVal 248  
 TGTGCAAGAGAAAGAGAGAGAGTTTCAAGAAAGTGTAATTGTGCTGTATCAACACTGT 300  
 TACTTTCGTACATTGGTAAAGTTTTTTTCTCTTCTTCTCTTTTCTTTTATTATA 360

FIG. 15D CONT.

CTTTAAGTTCTAGGGTACATGTGCACAATGTGCAGGTTTGTACGTA TGTTACATGTGC 420  
CATGTT 426

**FIG.16A**

-25  
 Human MKKTQTWILT CIYLQLLLEN PLVKTEGICR NRVTTNNVKDV TKLVANLPKD 25  
 Monkey MKKTQTWILT CIYLQLLLEN PLVKTEGICR NRVTTNNVKDV TKLVANLPKD  
 Dog MKKTQTWIIIT CIYLQLLLEN PLVKTKGICG KRVTDDVKDV TKLVANLPKD  
 Cat MKKTQTWIVT CIYLQXLLFN PLVKTKGLCR NRVTTDDVKDV TKLVANLPKD  
 Cow MKKTQTWIIIT CIYLQLLLEN PLVHTQGICS NRVTTDDVKDV TKLVANLPKD  
 Rat MKKTQTWIIIT CIYLQLLLEN PLVKTQEICR NPVTDNVKDI TKLVANLPKD  
 Mouse MKKTQTWIIIT CIYLQLLLEN PLVKTKEICG NPVTDNVKDI TKLVANLPND  
 Chicken TWIIIT CFCLQLLLEN PLVKAQSSCG NPVTDDVNDI AKLVGNLPND  
 Scfpep MKKTQTWIIIT CIYLQLLLEN PLVkt.giCr nrvTd.vkDv tKLVaNLpKd

26  
 Human YMITLKYVPG MDVLP SHCWI SEMVVQLSDS LTDLLDKFSN ISEG...LSN 72  
 Monkey YMITLKYVPG MDVLP SHCWI SEMVVQLSDS LTDLLDKFSN ISEG...LSN  
 Dog YKIALKYVPG MDVLP SHCWI SVMVEQLSVS LTDLLDKFSN ISEG...LSN  
 Cat YKIALKYVPG MDVLP SHCWI SVMVEQLSVS LTDLLDKFSN ISEG...LSN  
 Cow YMITLKYVPG MDVLP SHCWI SEMVEQLSVS LTDLLDKFSN ISEG...LSN  
 Rat YMITLNYVAG MDVLP SHCWL RDMVTHLSVS LTLLDKFSN ISEG...LSN  
 Mouse YMITLNYVAG MDVLP SHCWL RDMVIQLSLS LTLLDKFSN ISEG...LSN  
 Chicken YLITLKYVPG MDVLP SHCWL HLMVPEFSRS LHNLLQKFSN ISEG...LSN  
 Scfpep YmitLkYVpg MDvLpShCwi semveqlsvs LtDLLdKFSn Iseg...LSN

73  
 Human YSIIDKLvNI VDDLVECVKE NSSKD.LKKS FKSPePrLFT PEEFFRIFNR 121  
 Monkey YSIIDKLvNI VDDLVECVKE NSSKD.LKKS FKSPePrLFT PEEFFRIFNR  
 Dog YSIIDKLvKI VDDLVECTEG YSFEN.VKKA PKSPeLrLFT PEEFFRIFNR  
 Cat YSIIDKLvKI VDDLVECVEG HSSEN.VKKS SKSPePrLFT PEEFFRIFNR  
 Cow YCIIDKLvKI VDDLVECMEX HSSEN.VKKS SKSPePrLFT PEEFFRIFNR  
 Rat YSIIDKLgKI VDDLVLcMEE NAPKN.VKES LKKPeTrNFT PEEFFSIFNR  
 Mouse YSIIDKLgKI VDDLVLcMEE NAPKN.VKES LKKPeTrNFT PEEFFSIFNR  
 Chicken YSIINNLTRI INDLMAcLAF DKNKDFIKEN GHLYEEDRFI PENFFRLFNS  
 Scfpep YsiIdkLvKi vDdLvEc.ee nsskn.vKks .kspePrLft PEEFFrIFnr

# FIG.16B

122 Human SIDAfKDF.V VASeTSDCVV SSTL.SPEKD SRVSVTKPFM LPPVAASSLR 169  
 Monkey SIDAfKDF.A VASeTSDCVV SSTL.SPEKD SRVSVTKPFM LPPVAASSLR  
 Dog SIDAfKDLET VASKSSECvV SSTL.SPDKD SRVSVTKPFM LPPVAASSLR  
 Cat SIDAfKDLEM VASKTSECvV SSTL.SPEKD SRVSVTKPFM LPPVAASSLR  
 Cow SIDAfKDLEI VASKMSECvI SSTs.SPEKD SRVSVTKPFM LPPVAASSLR  
 Rat SIDAfKDF.M VASDTSDCVL SSTL.GPEKD SRVSVTKPFM LPPVAASSLR  
 Mouse SIDAfKDF.M VASDTSDCVL SSTL.GPEKD SRVSVTKPFM LPPVAASSLR  
 Chicken TIEVYKEFAD SLdK.NdCIm PSTVETPEND SRVAVTKTIS FPPVAASSLR  
 Scfpep sIdafKdf.m vaektSDCvV SSTL.sPeKD SRVSVTKPfm LPPVAASSLR

170 Human NDSSSSNRKA KNPPGD..... SSLHWAAM ALPAFFSLII GFaFGALYWK 213  
 Monkey NDSSSSNRKA KNPTGD..... SSLHWAAM ALPAFFSLII GFaFGALYWK  
 Dog NDSSSSNRKA SNSIGD..... SNLQWAAM ALPAFFSLVI GFaFGALYWK  
 Cat NDSSSSNRKX TNPIED..... SSIQWAVM ALPAFFSLVI GFaFGALYWK  
 Cow NDSSSSNRKA SNSIED..... SSLQWAAV ALPAFFSLVI GFaFGALYWK  
 Rat NDSSSSNRKA AKSPED..... PGLQWTAM ALPALISLVI GFaFGALYWK  
 Mouse NDSSSSNRKA AKAPED..... SGLQWTAM ALPALISLVI GFaFGALYWK  
 Chicken NDSIGSNTSS NSNKEALGFI SSSSLQGISI ALTSLLSLLI GFILGAIYWK  
 Scfpep NDSSssNRka .n..ed..... sslqwaam ALpalfSLVI GFaFGALYWK

214 Human KRQPSLTRAV ENIQIN...E EDNEISMLQe KEREfQeV 248  
 Monkey KRQPSLTRAV ENIQIN...E DDNEISMLQe KEREfQeV  
 Dog KKQPNLTRTV ENIQIN...E EDNEISMLQe KEREfQeV  
 Cat KKQPNLTRTV ENIQIN...E EDNEISMLQe KEREfQeV  
 Cow KKQPNLTRTV ENRQIN...E EDNEISMLQe KEREfQeV  
 Rat KKQSSLTRAV ENIQIN...E EDNEISMLQe KEREfQeV  
 Mouse KKQSSLTRAV ENIQIN...E EDNEISMLQe KEREfQeV  
 Chicken KTHPKSRPES NETIQCHGCQ EENEISMLQe KEKEHLQV  
 Scfpep Kkqpeltrav eniqin...e edNEISMLQe KEREfQeV

FIG. 16C

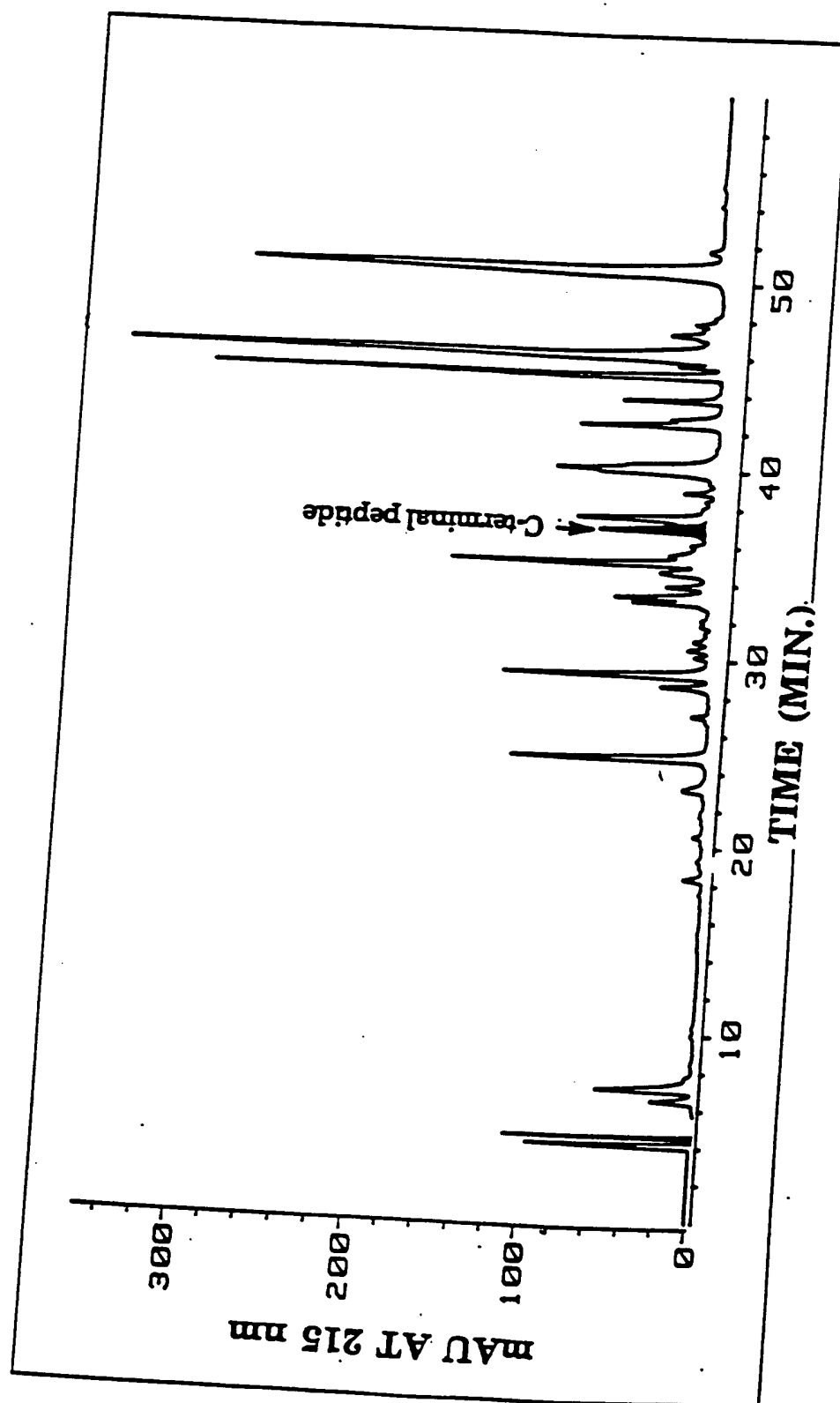




FIG. 16D

EcoRI

ta a t t t a a t t c g t a  
GAATTCTTCCGTATCTTCAACCGTTCCATCGACGCTTTCAAAGACTTCGTT  
 E F F R I F N R S I D A F K D F V

g a t tagt t t g t a at a ag t g  
 GTTGCTTCCGAAACCTCCGACTGCGTTGTTTCCTCCACCCTGTCTCCGGAA  
 V A S E T S D C V V S S T L S P E

BstEII

t a a cagt c a a t t a c t . a  
 AAAGACTCCC GTGTTTCGGTTACCAAACCGTTTCATGCTGCCGCCGGTTGCT  
 K D S R V S V T K P F M L P P V A

cag tag t ag agtag agt tagt g a t  
 GCTTCCTCCCTGCGTAACGACTCCTCCTCCTCCAACCTCCAAATACATCTAC  
 A S S L R N D S S S S N S K Y I Y

BamHI

t  
CTGATCTAATAGGATCC  
 L I . .

FIG 16E

BstEII  
GGTTACCAAACCGTTCATGCTGCCGCCGGTTGCTGCTTAATAGGATCC BamHI  
V T K P F M L P P V A A . .

FIG.17

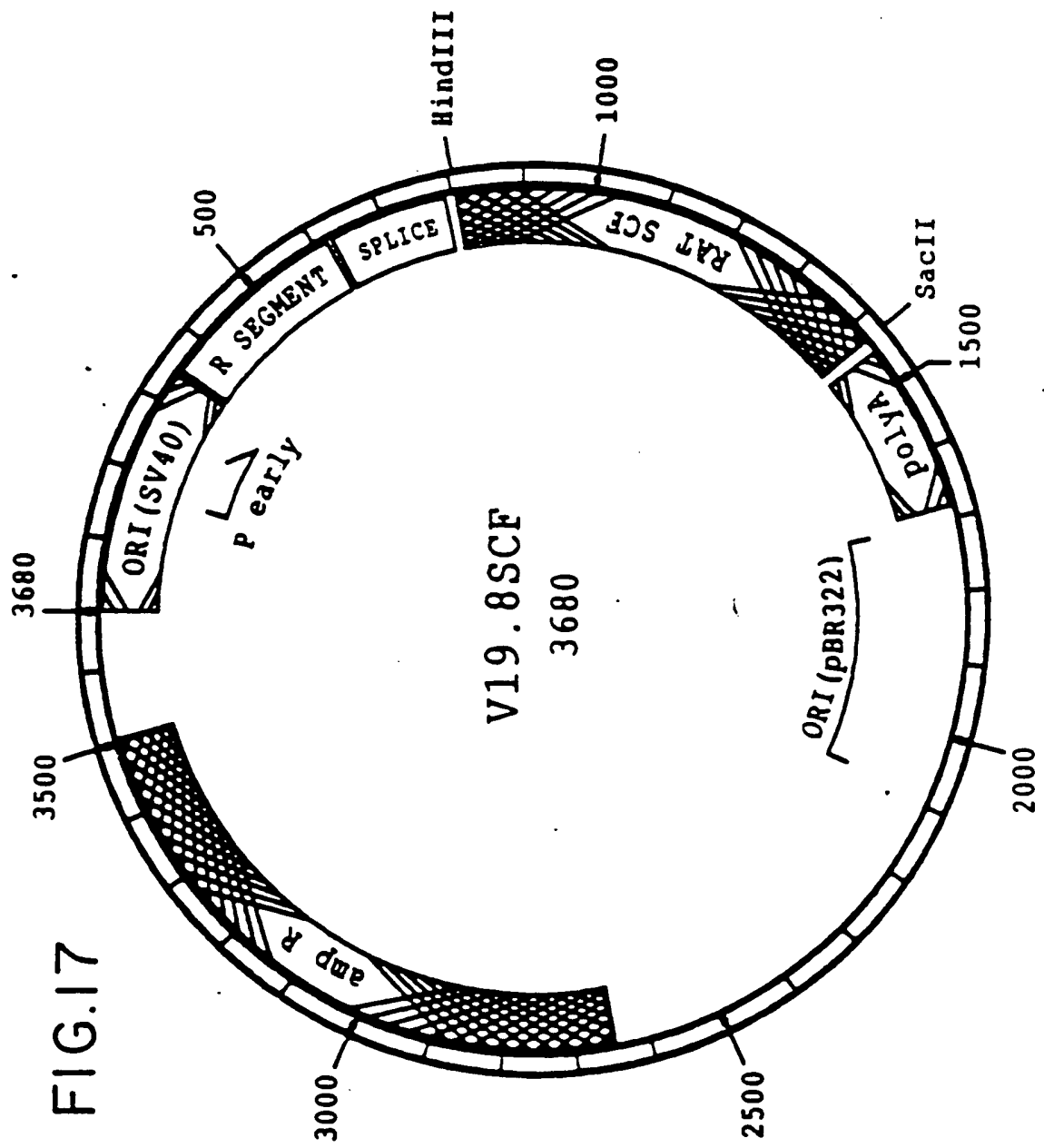
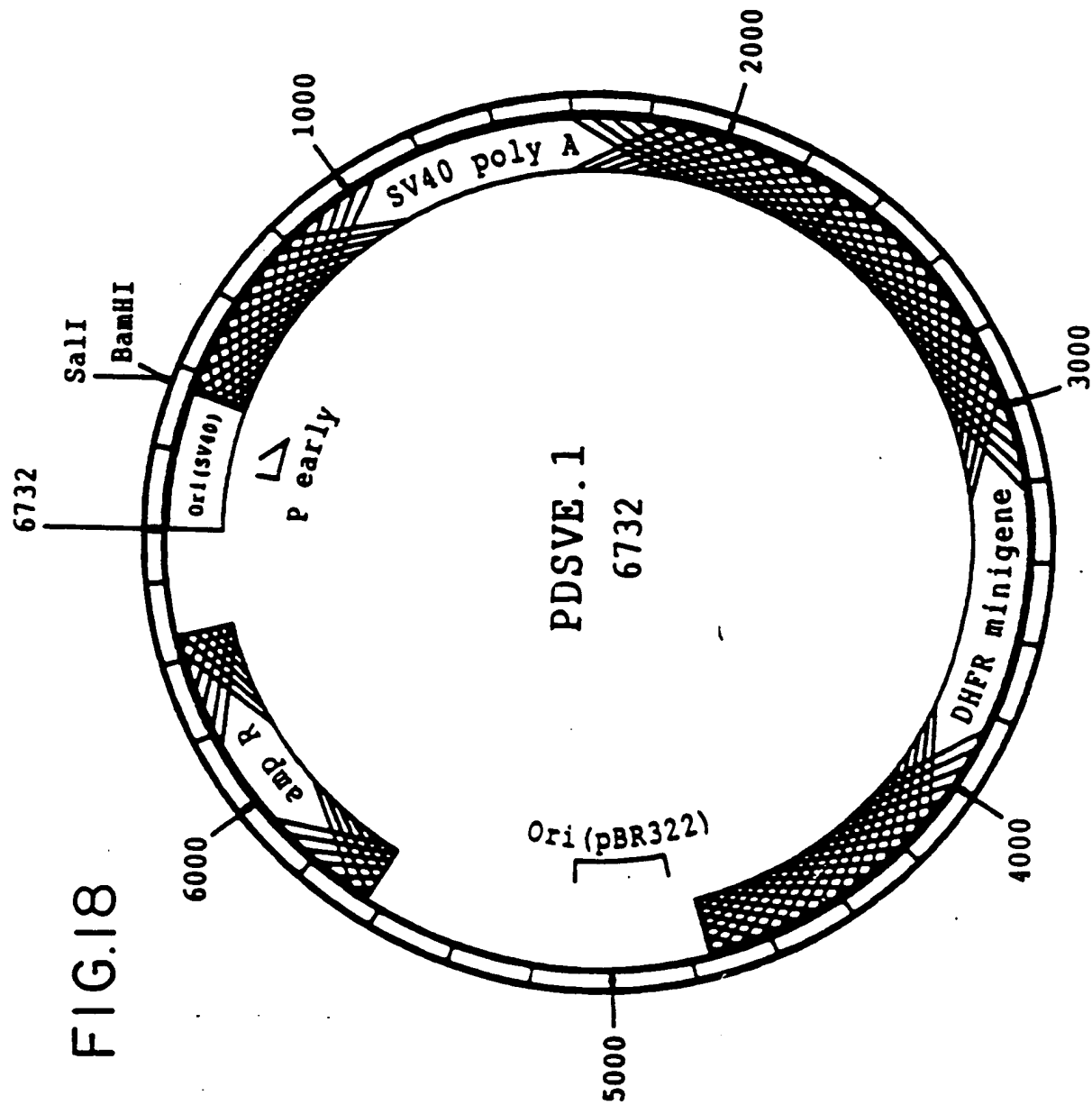


FIG.18



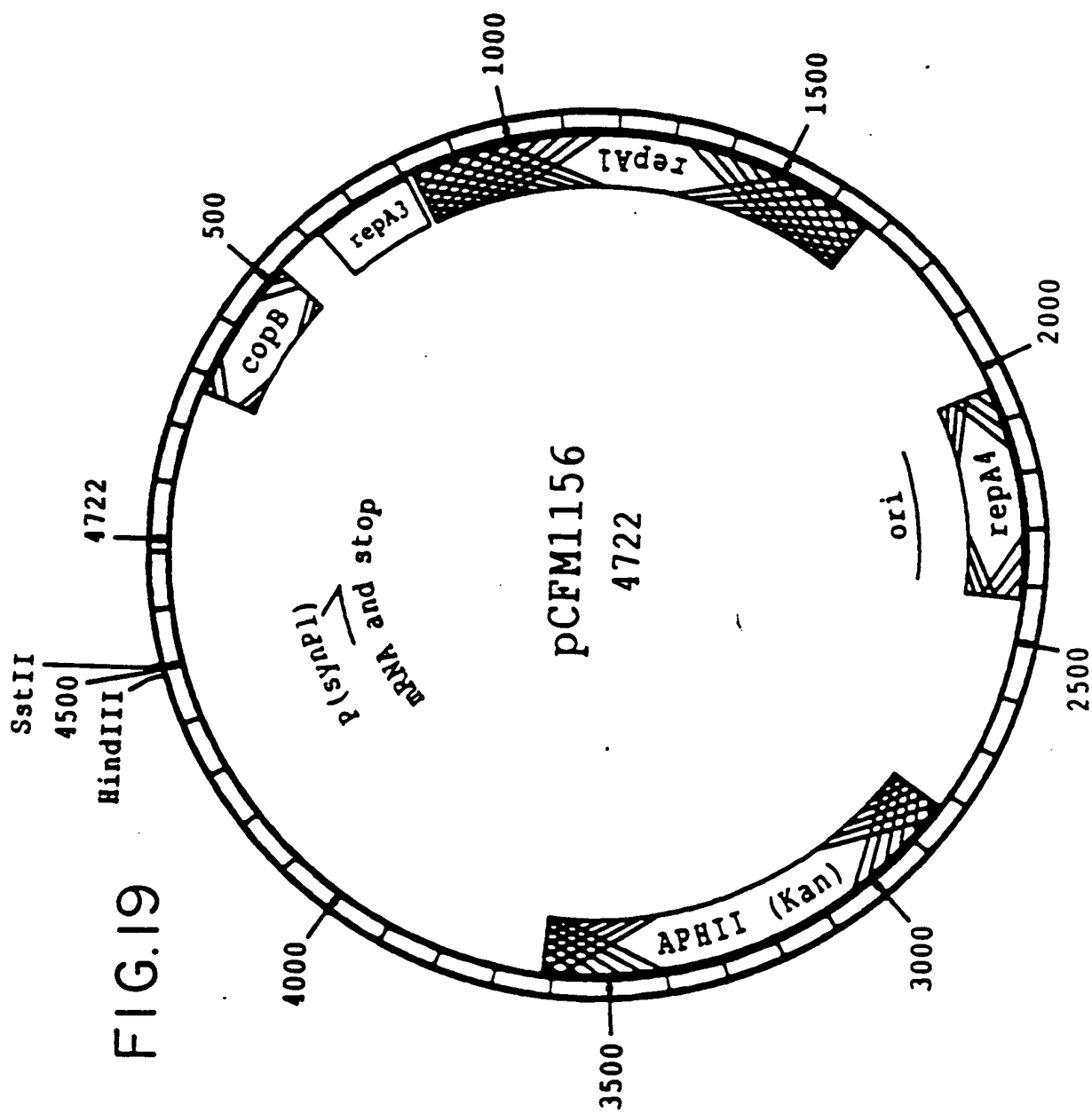


FIG.19

FIG.20A

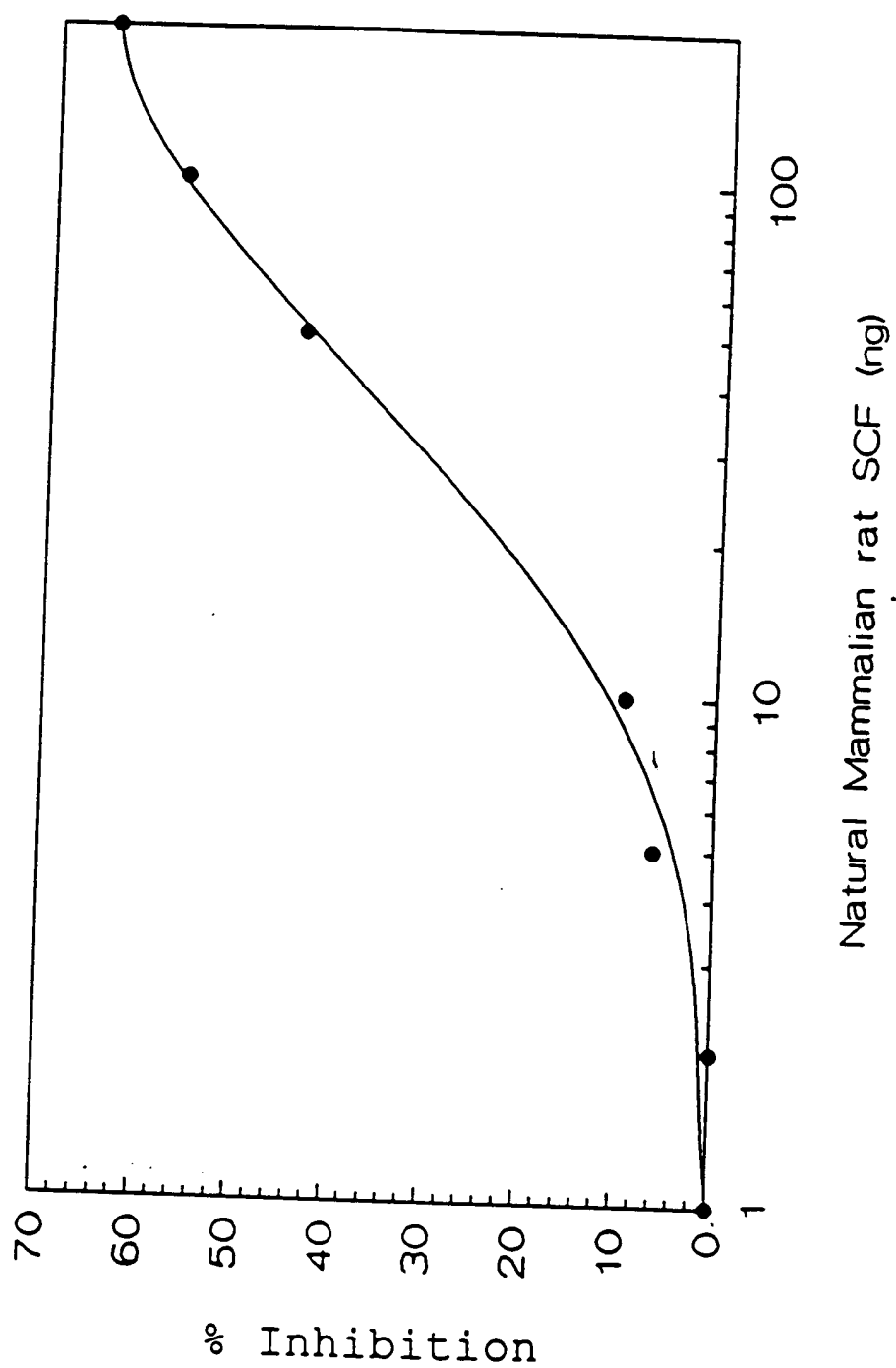


FIG.20B

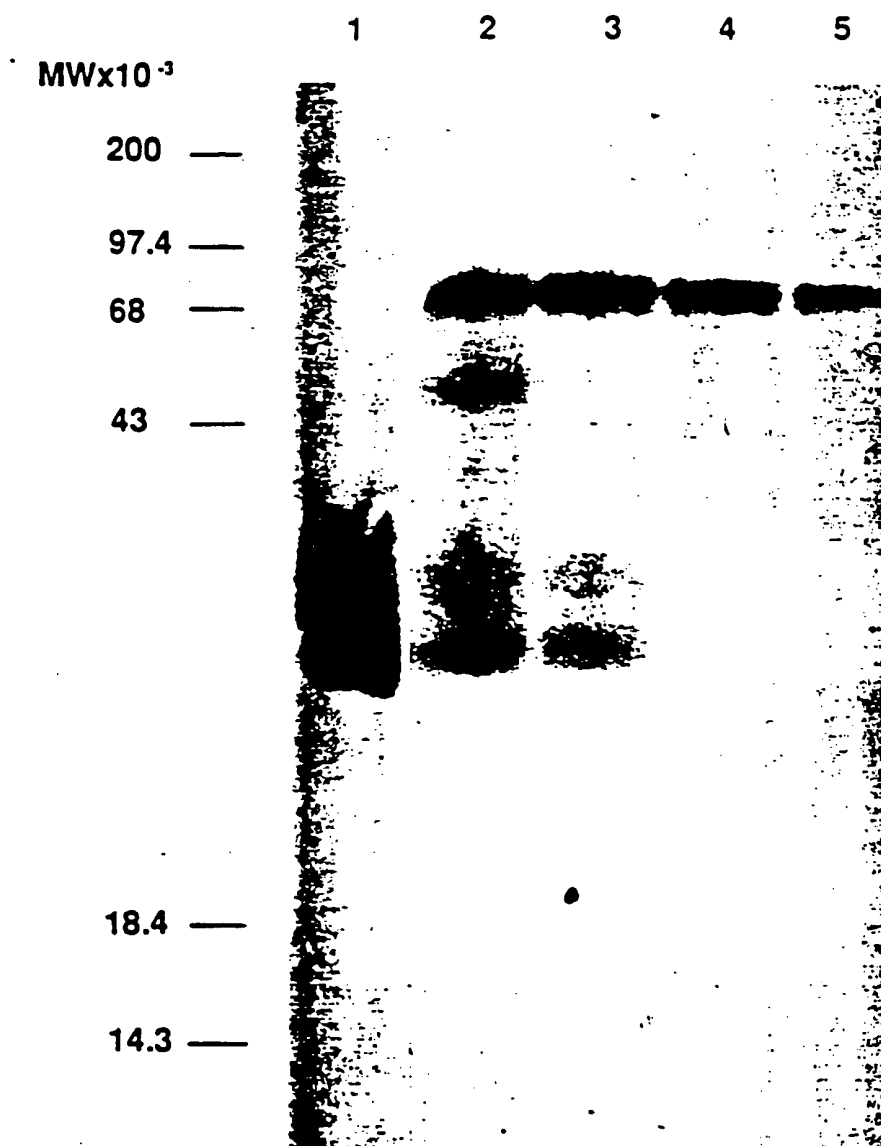


FIG. 21

1 2 3 4 5 6 7 8 MWx10<sup>-3</sup>



— 43

— 29

— 18.4

— 14.3

— 6.2



FIG.22

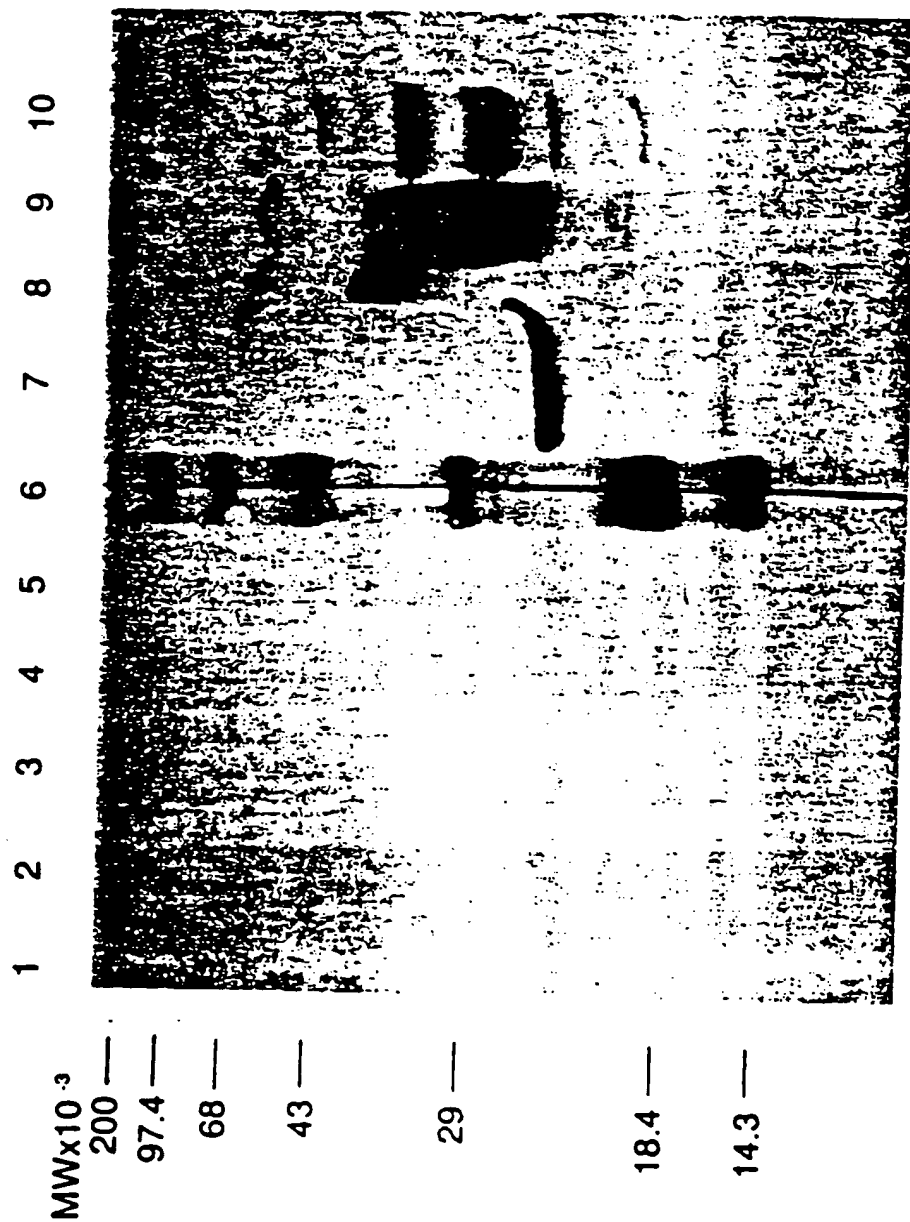


FIG. 22A

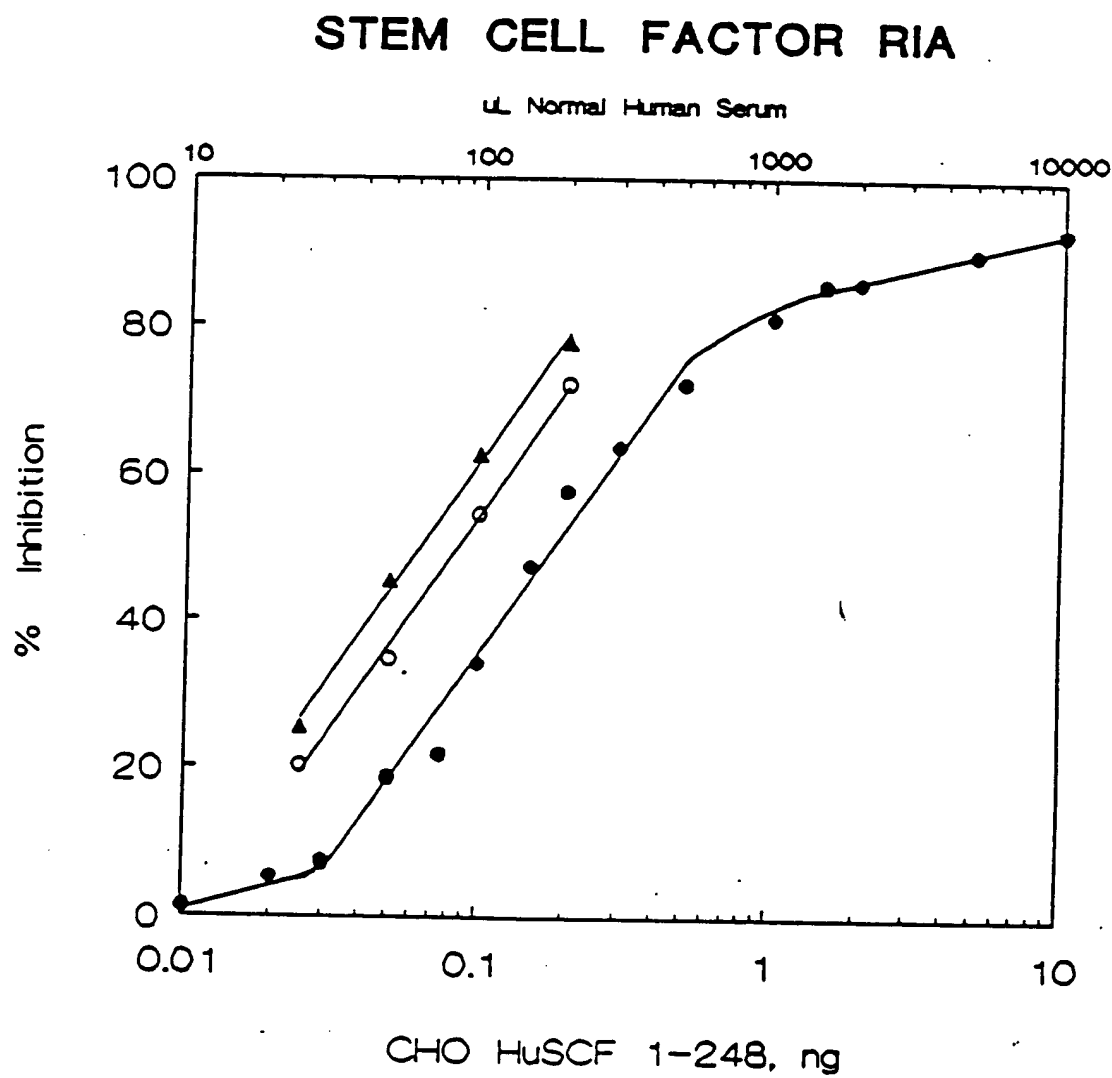
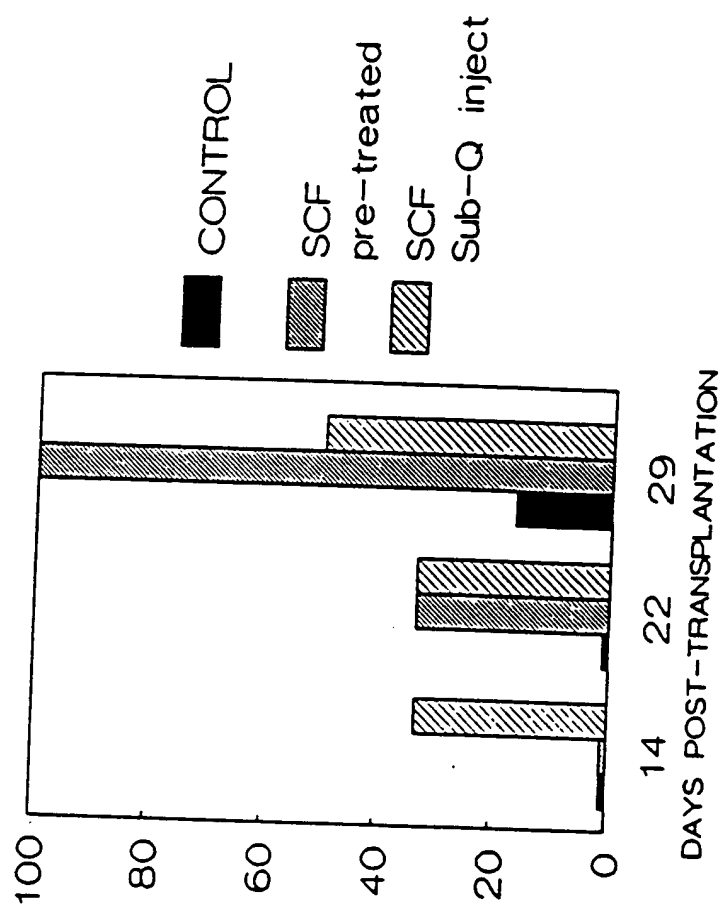


FIG. 23



% MICE CONVERTED TO DONOR PHENOTYPE

FIG. 24A

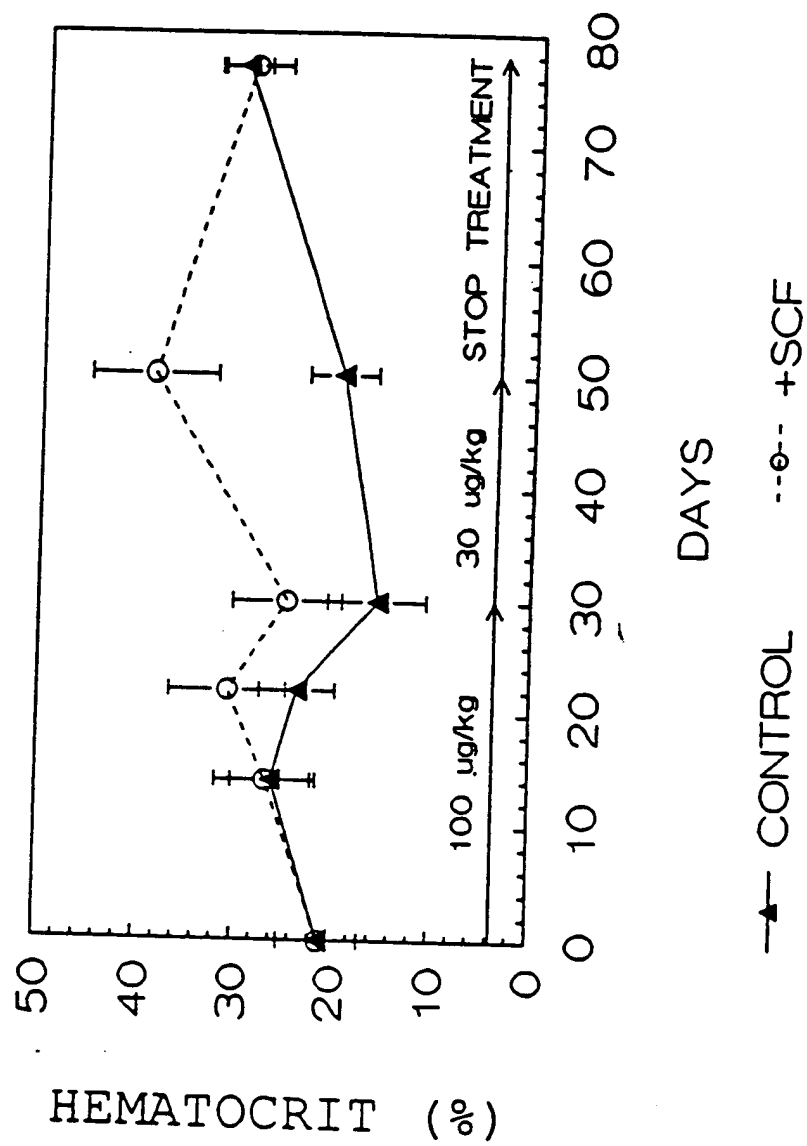
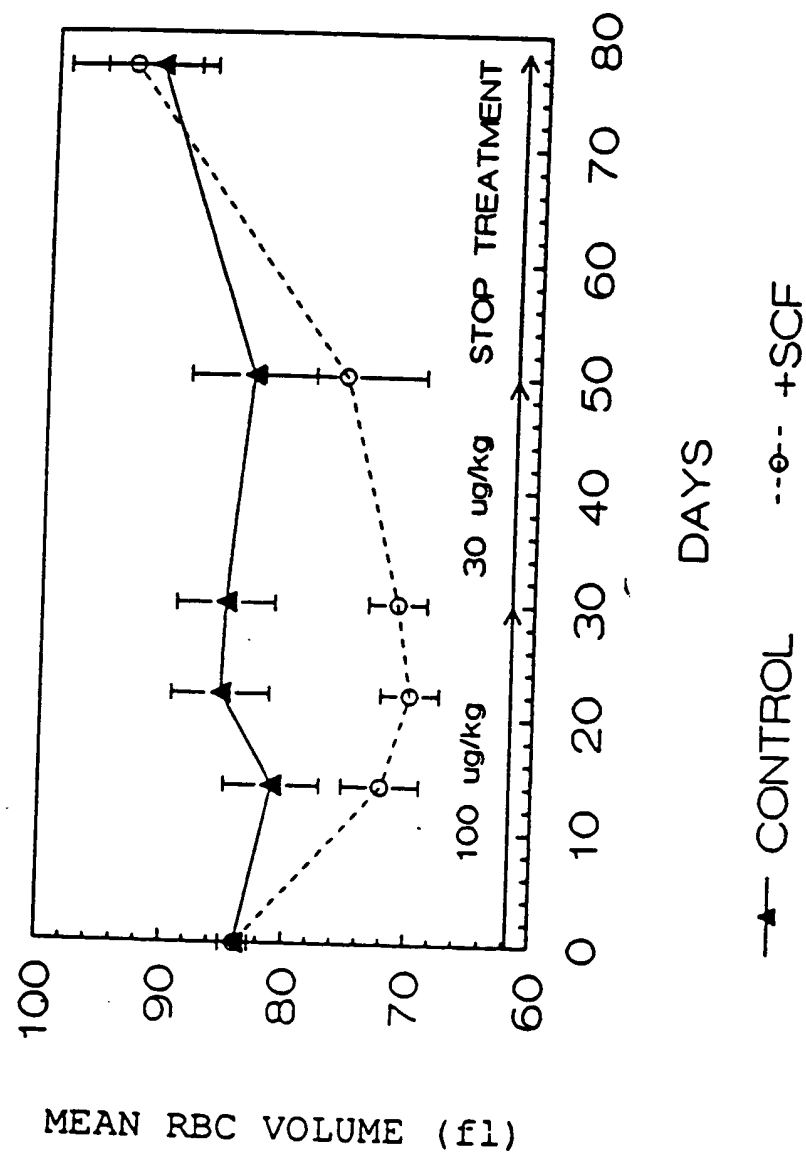
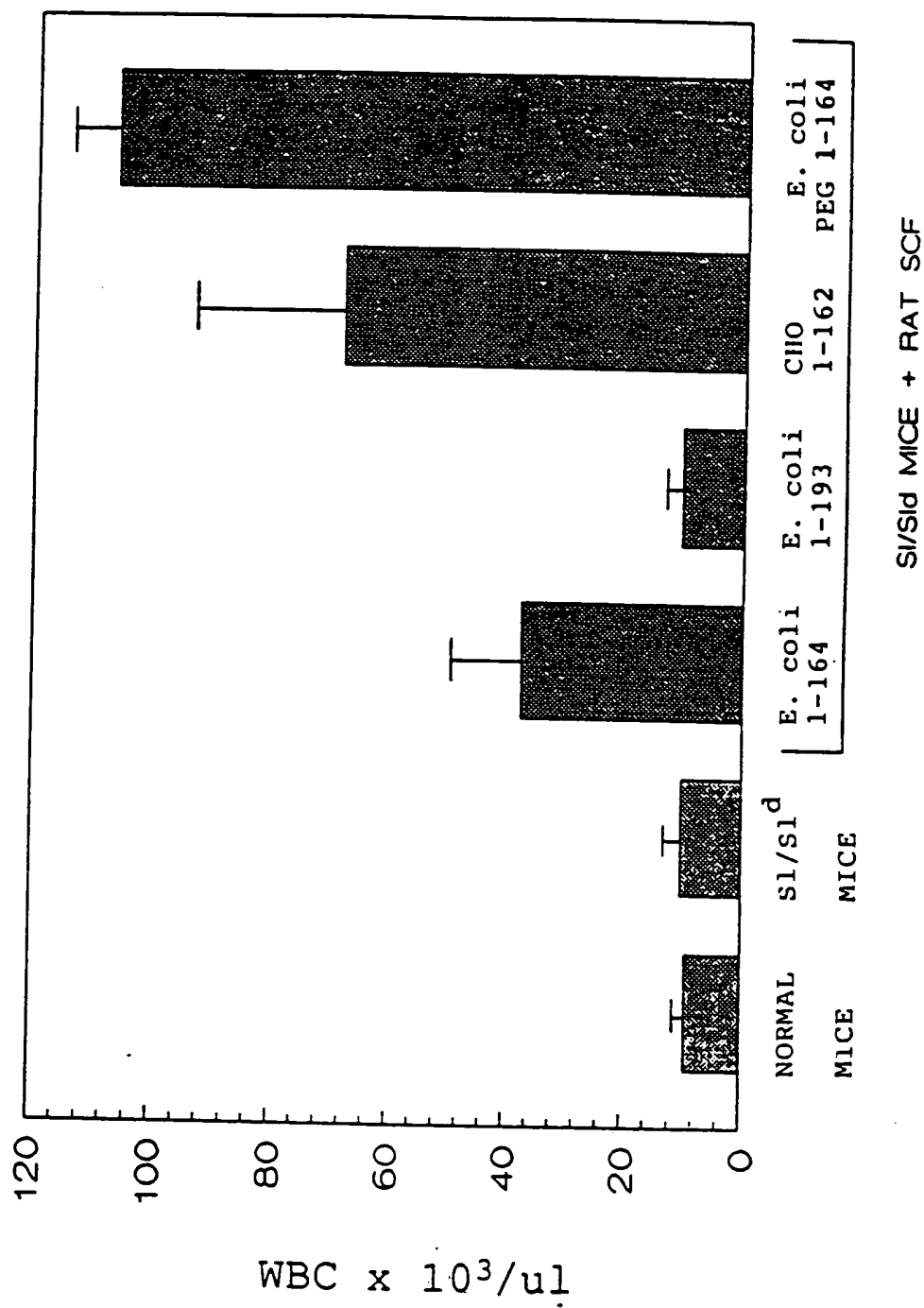


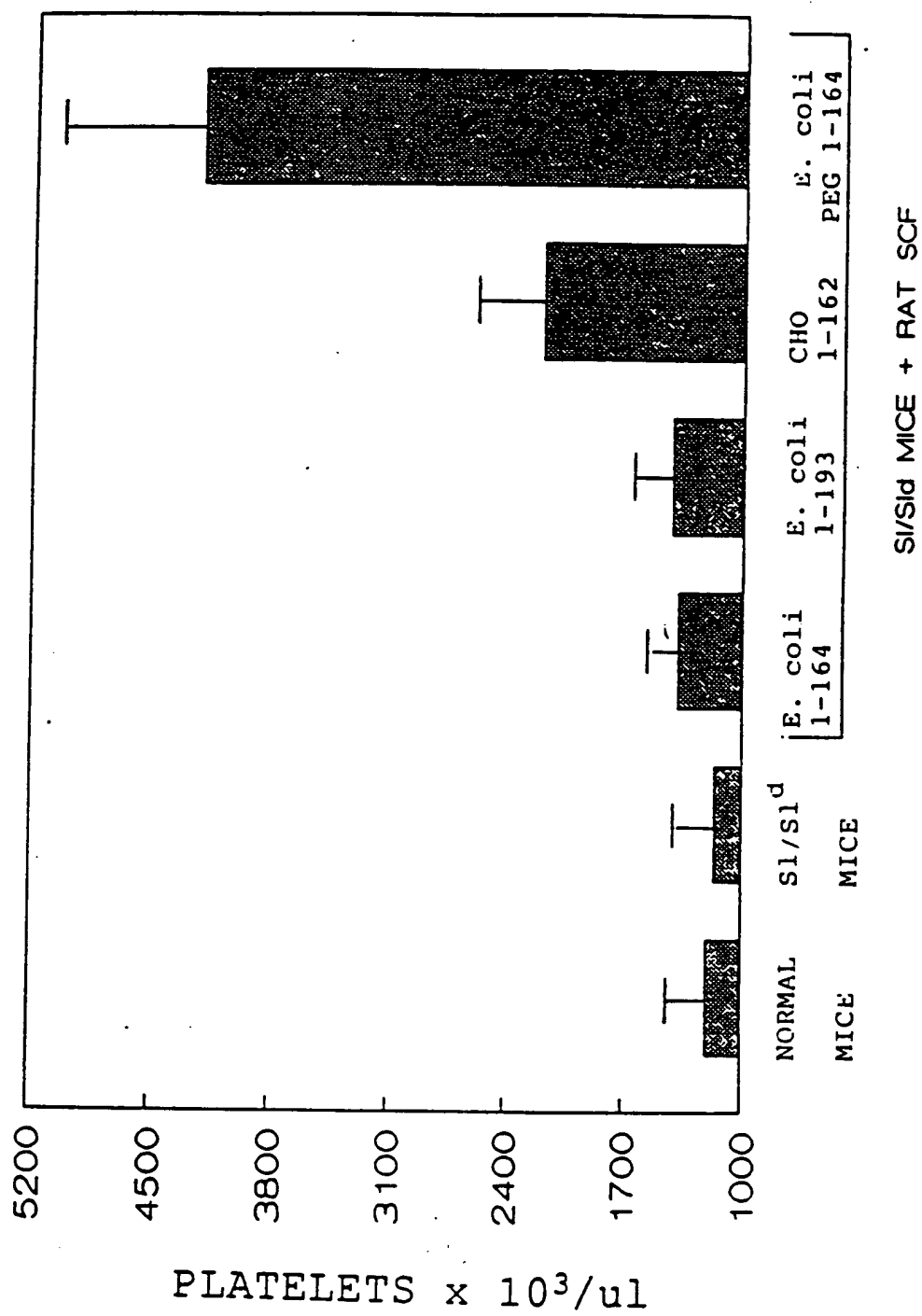
FIG. 24B



# FIG. 25



# FIG.26



# FIG. 27

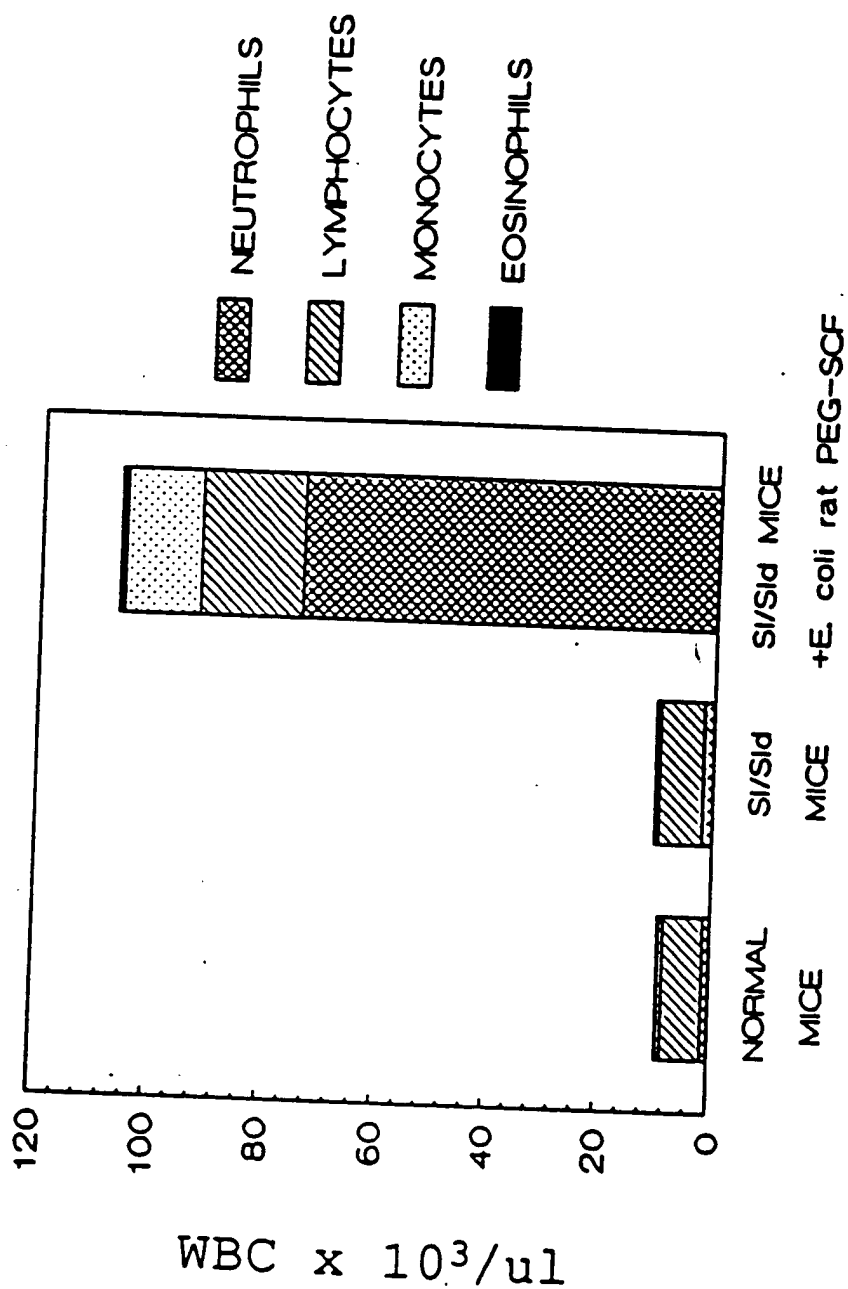




FIG. 28

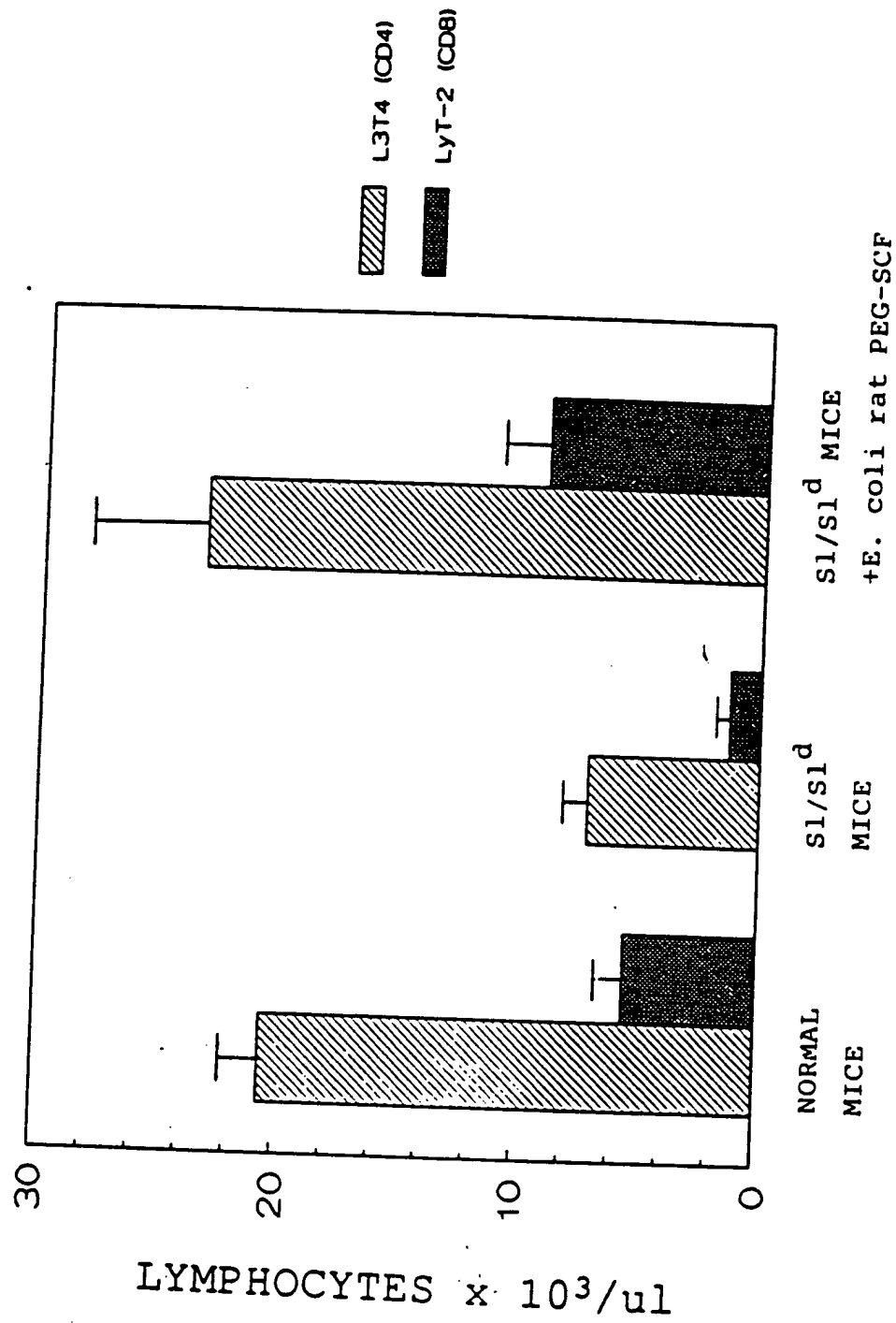
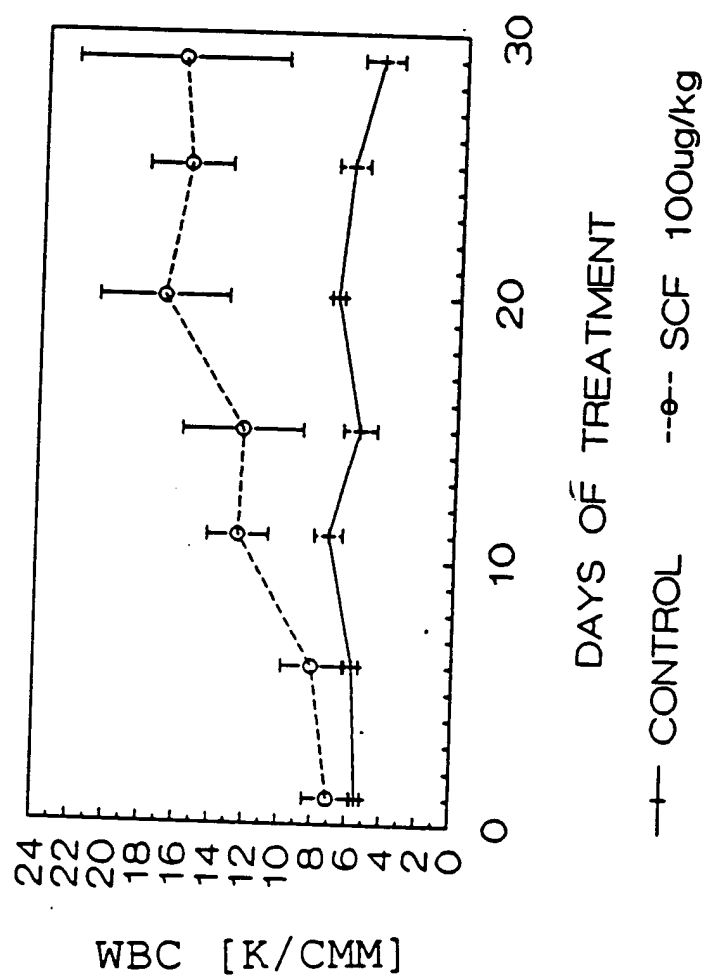


FIG.29A



# FIG. 29B

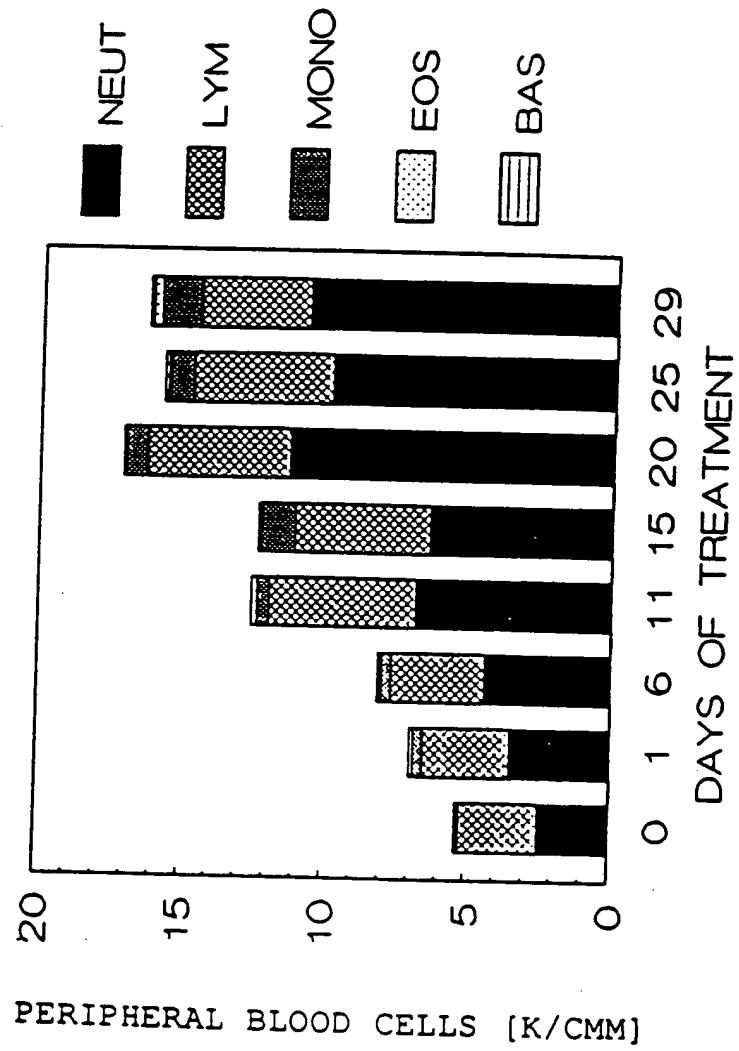


FIG.30A

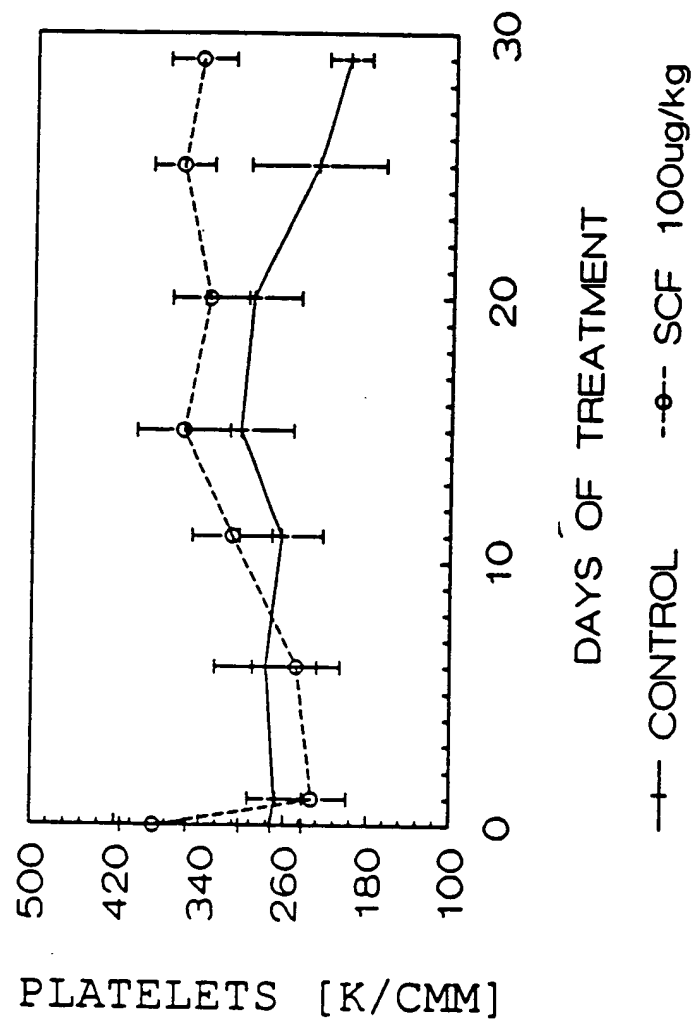


FIG. 30B

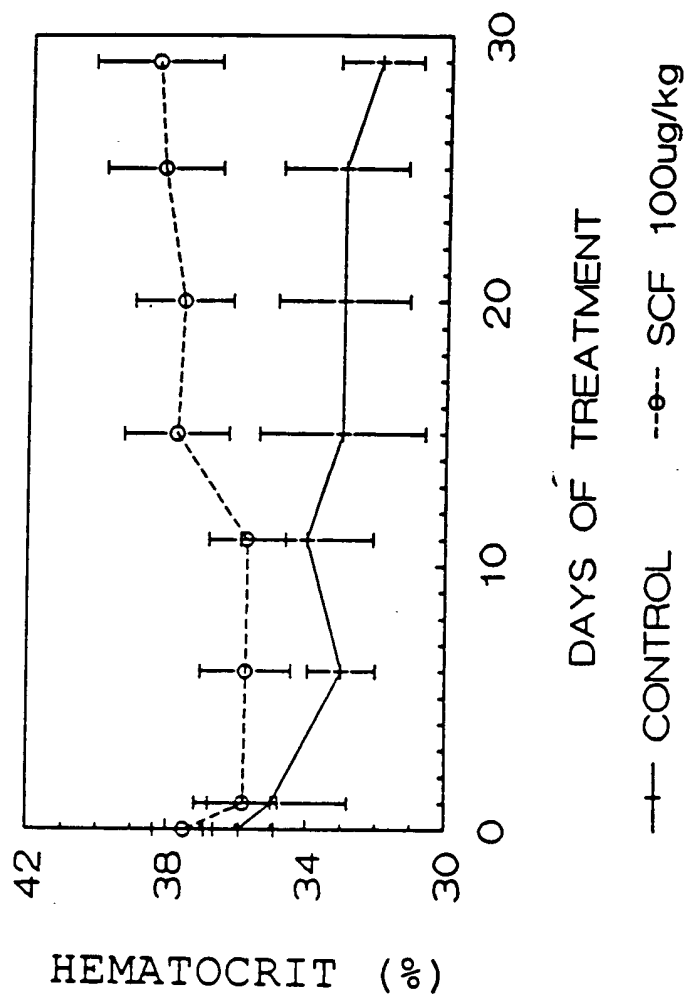


FIG. 31A

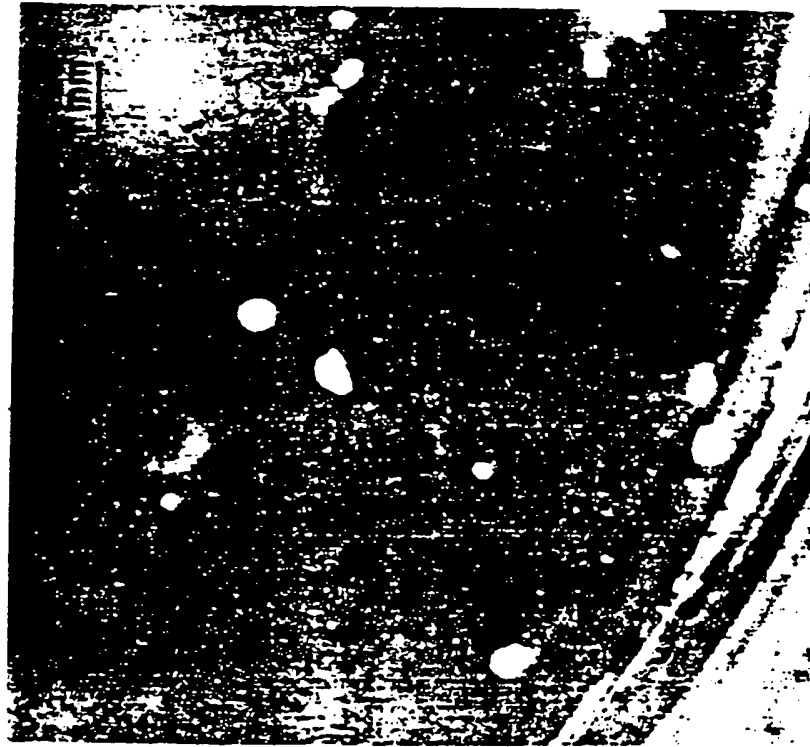


FIG. 31B

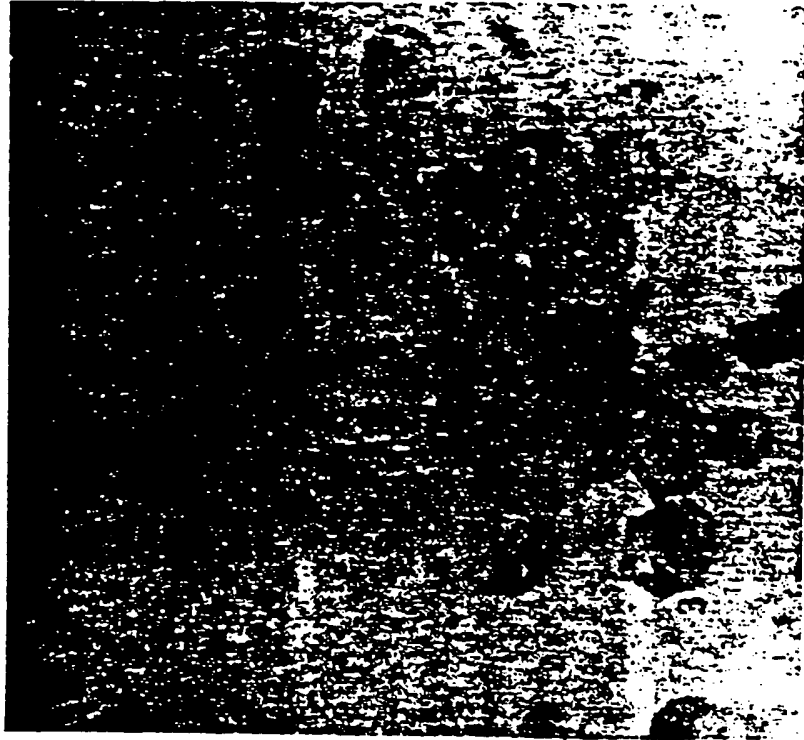
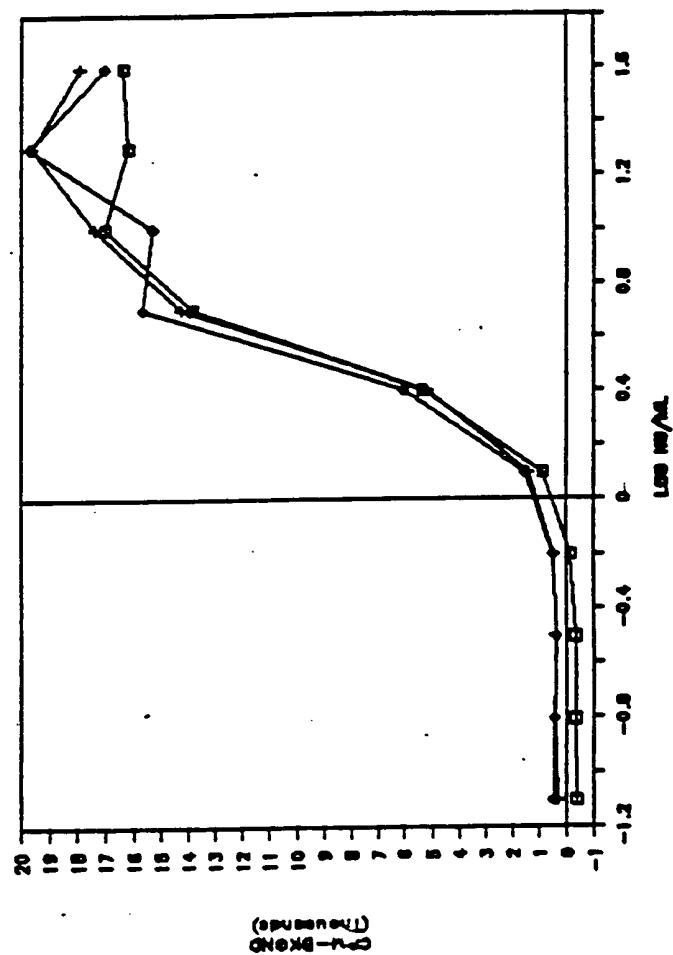


FIG. 31C

SCF4 SMP4



S Sephrose Load

FIG. 32A

11 15 19 23 27 31 35 37



97.4 —

66.2 —

42.7 —

31.1 —

21.5 —

14.4 —



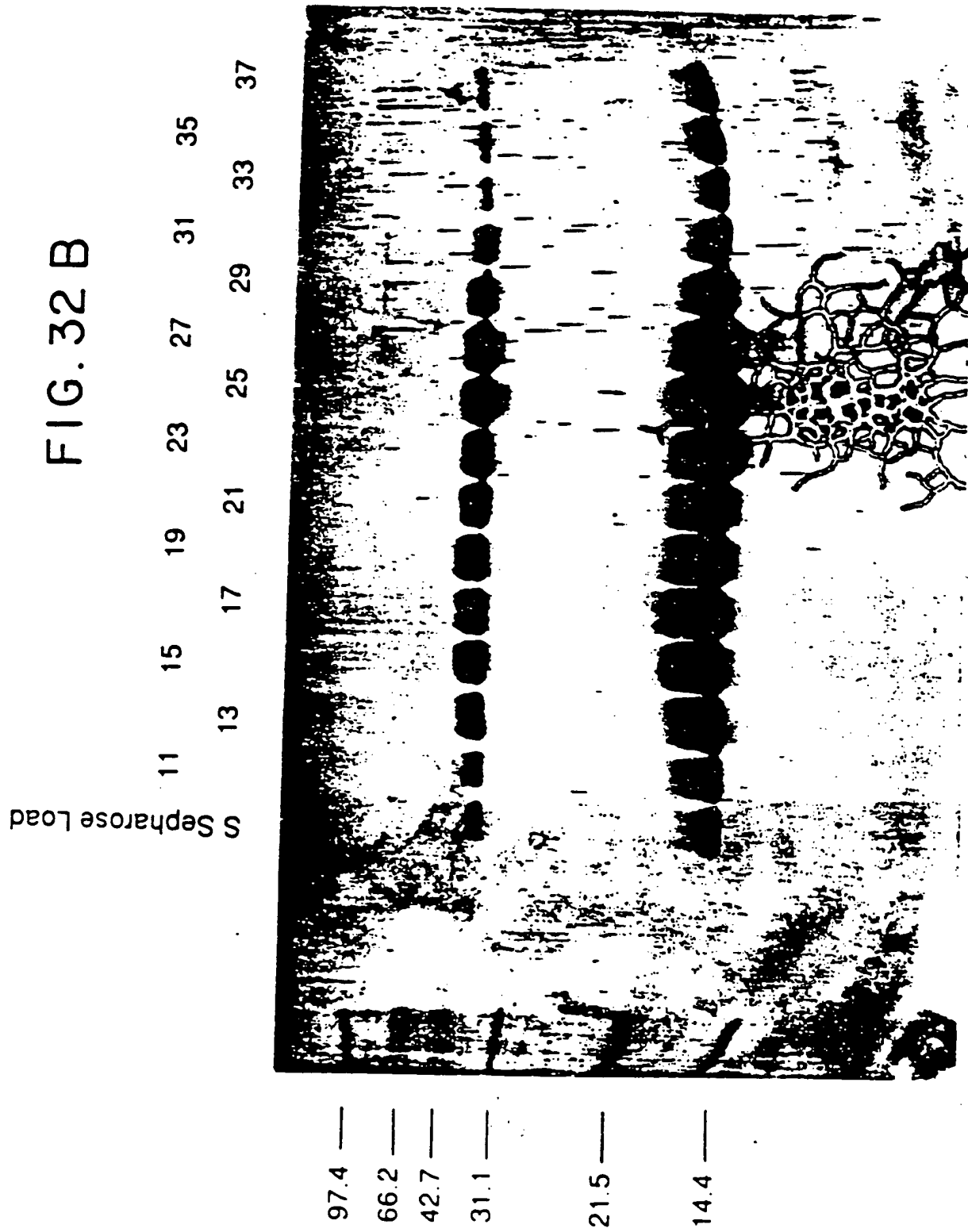
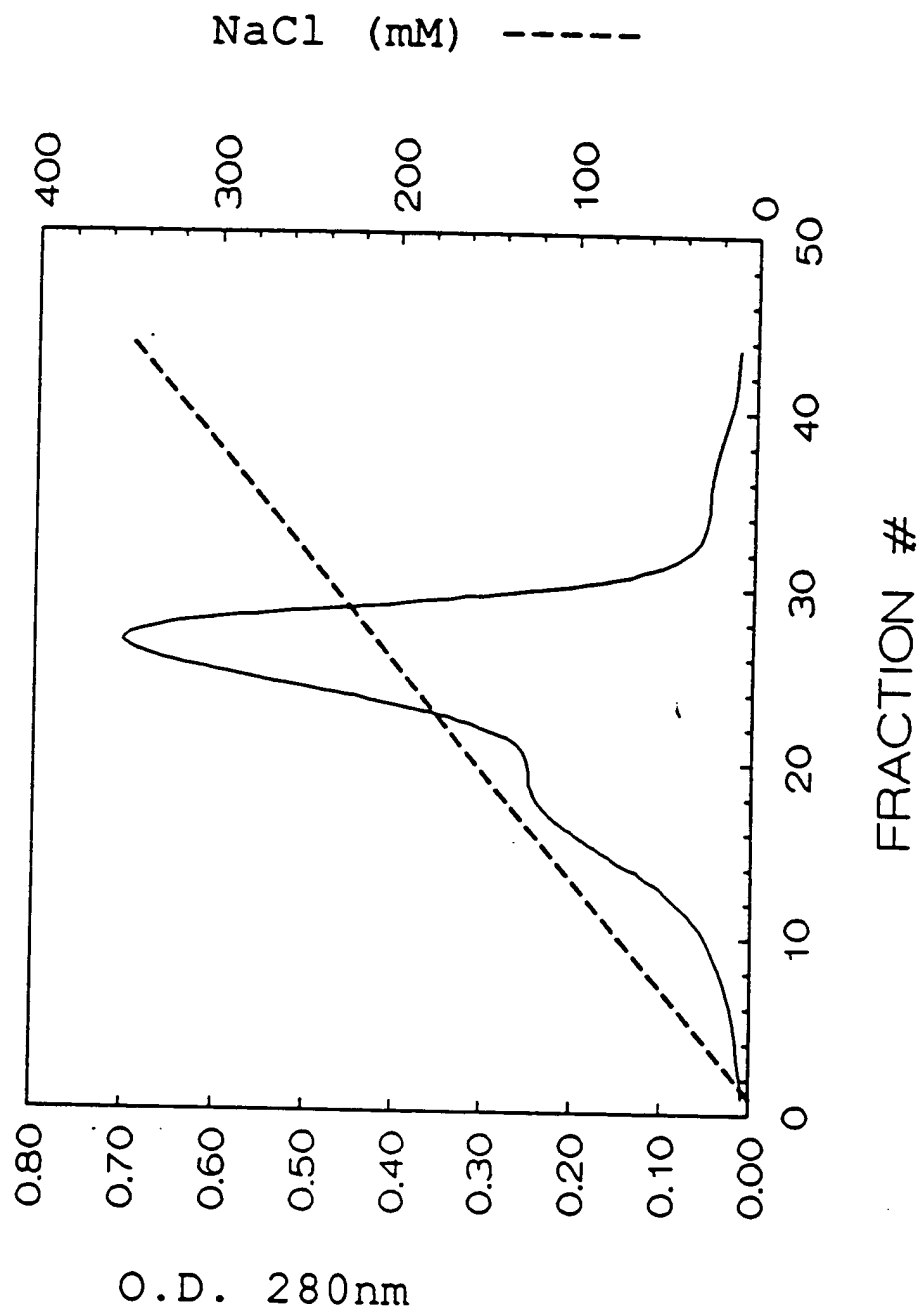


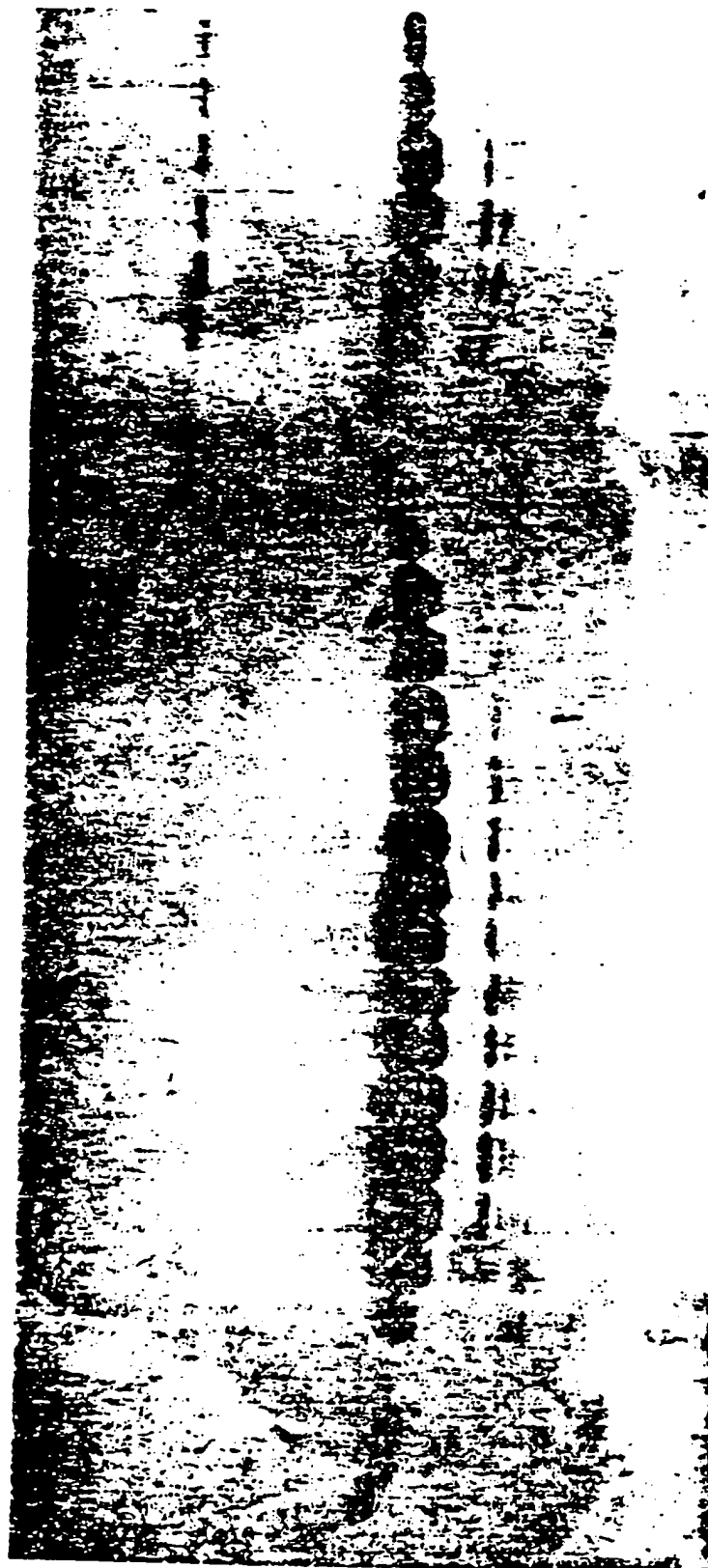
FIG. 33



# FIG. 34A

S Sepharose Pool  
C4 Load  
C4 Flow Thru

62	76	90	104	111	125	139	146	153	181	206	211	221	231
69	83	97											



97.4  
66.2  
42.7  
31.1  
21.5  
14.4

# FIG. 34B

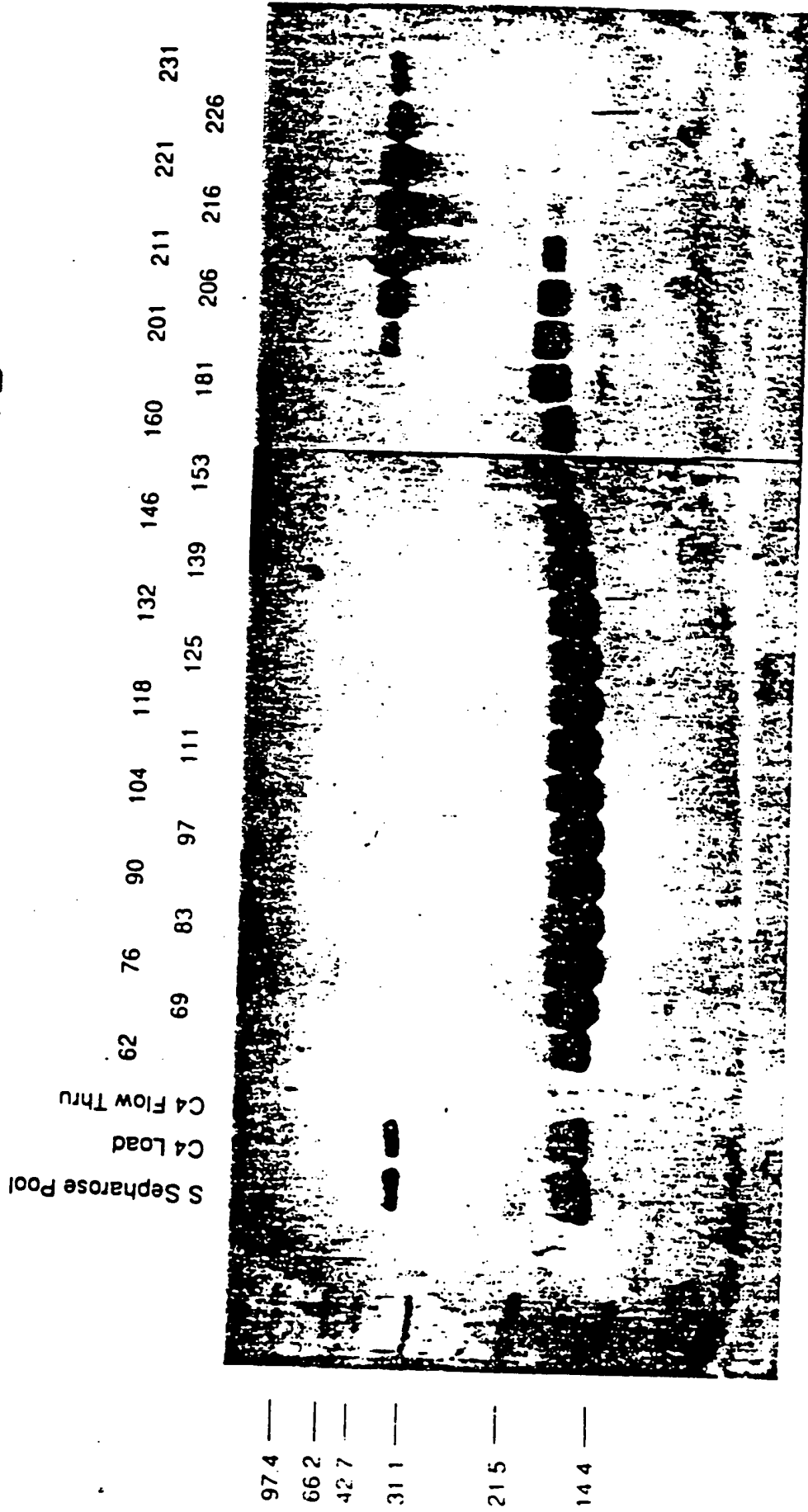


FIG. 35

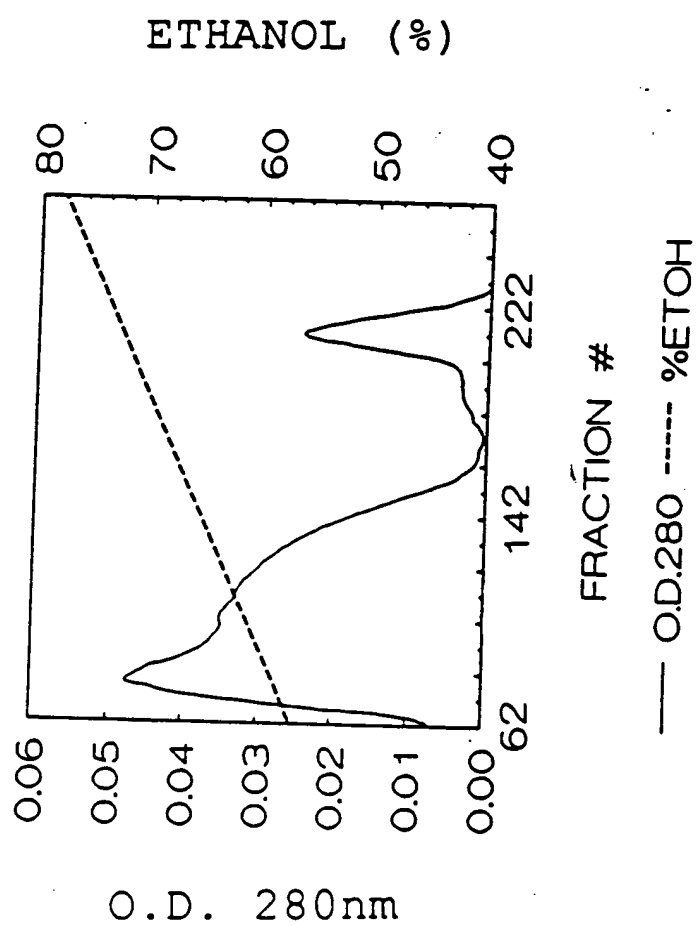
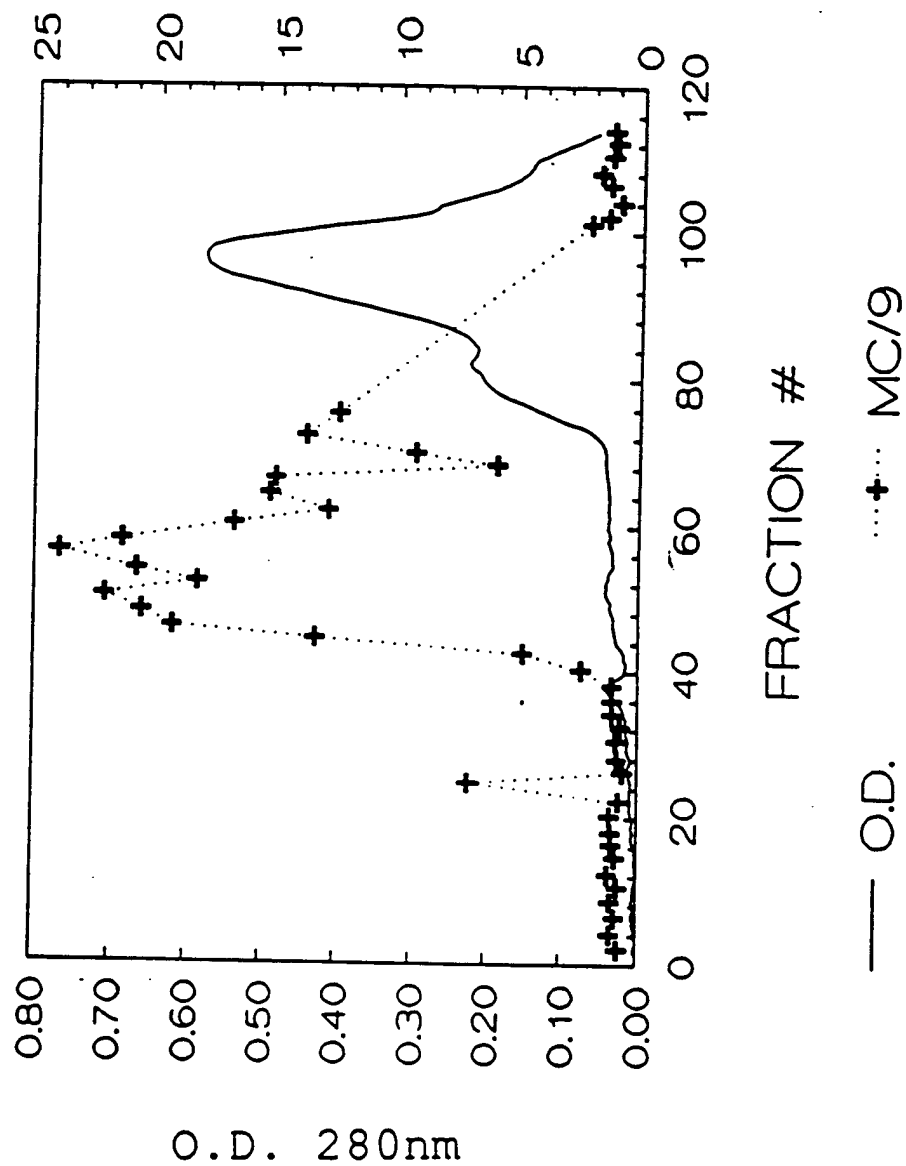


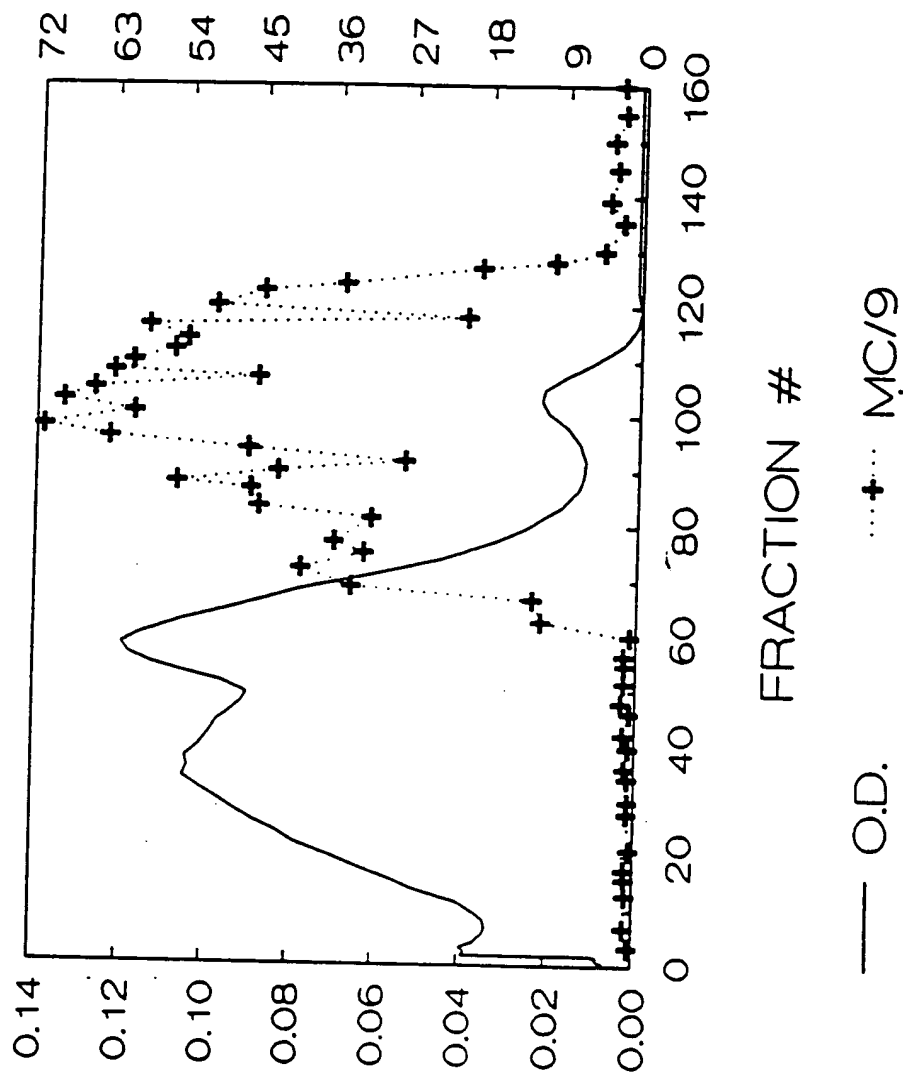
FIG. 36

MC/9 CPM ( $\times 10^{-3}$ )



# FIG. 37

MC/9 CPM ( $\times 10^{-3}$ )



O.D. 280nm ( $\times 10^1$ )

FIG. 39

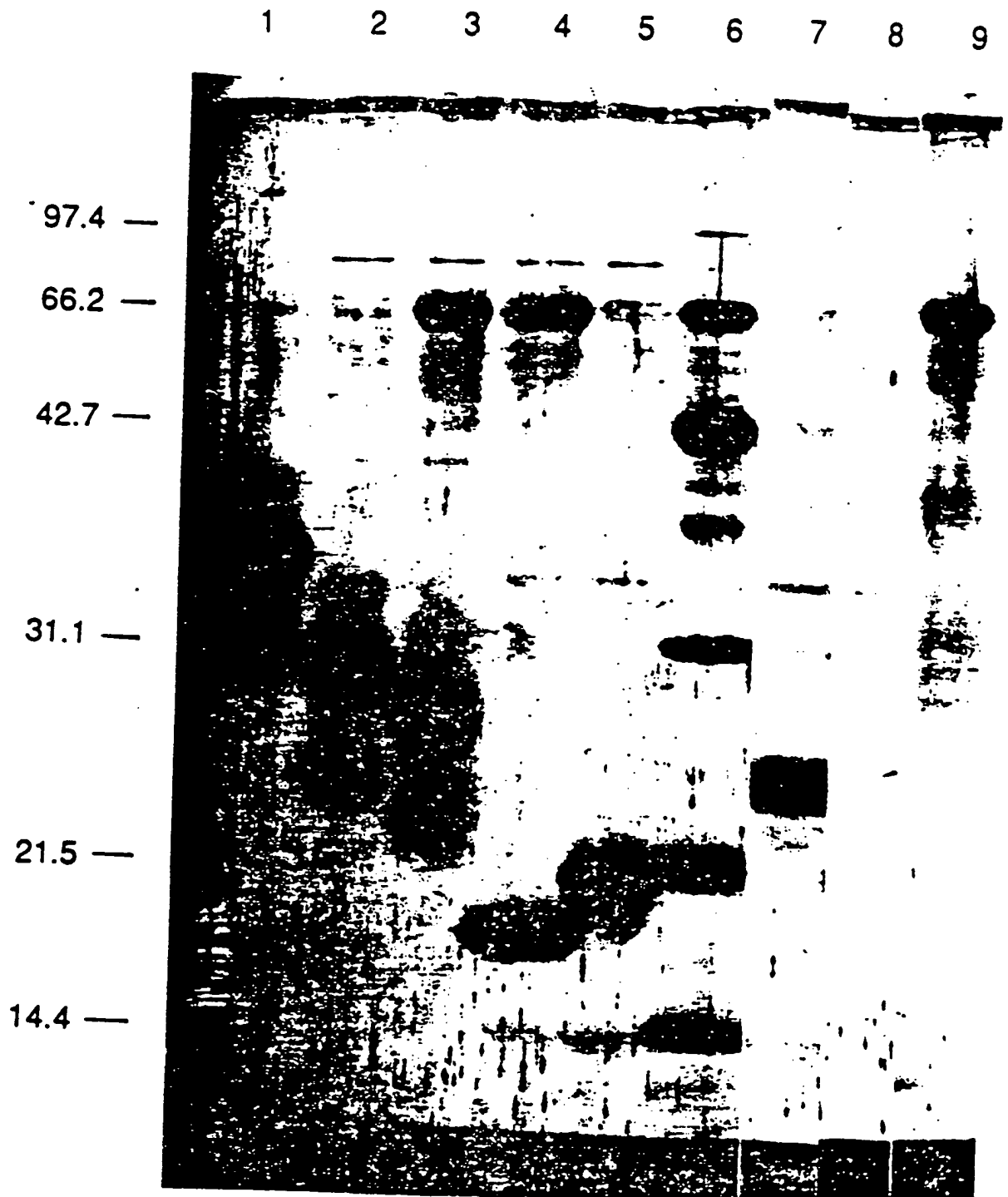




FIG. 40A

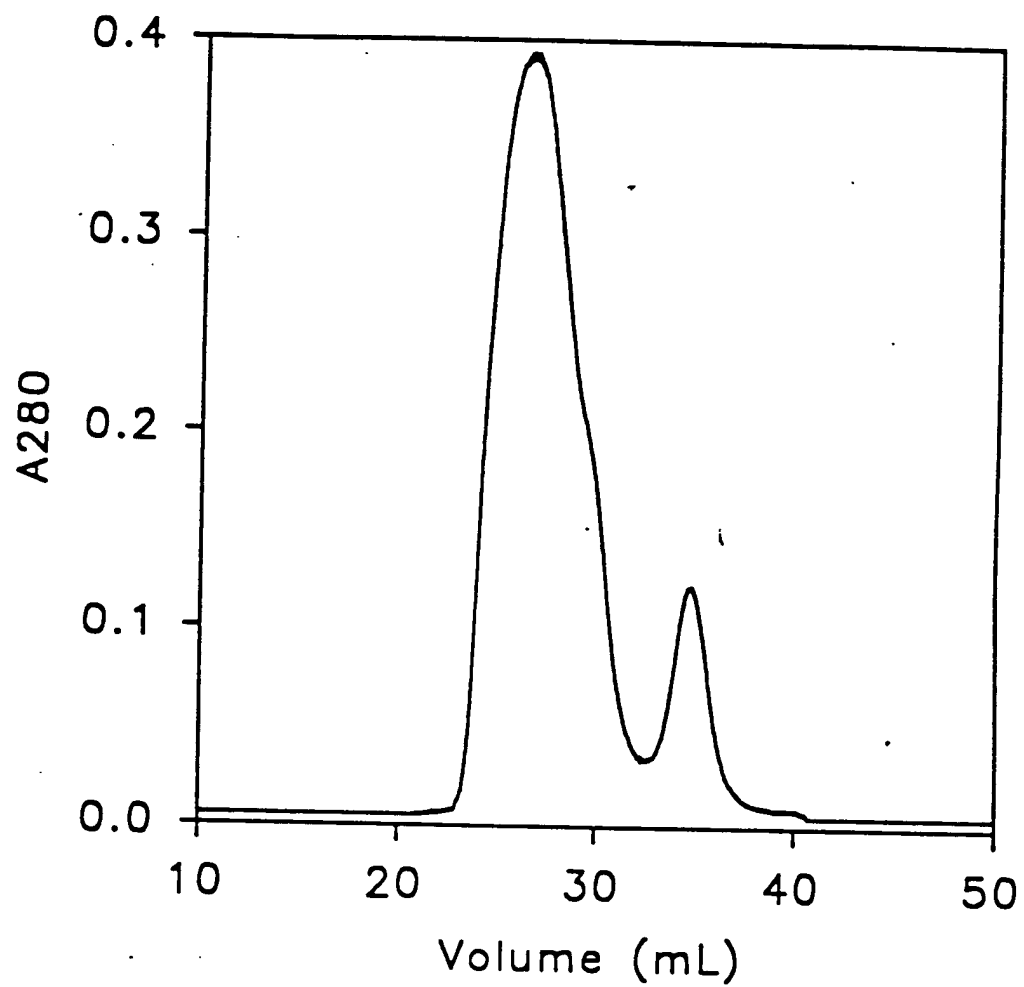


FIG. 40B

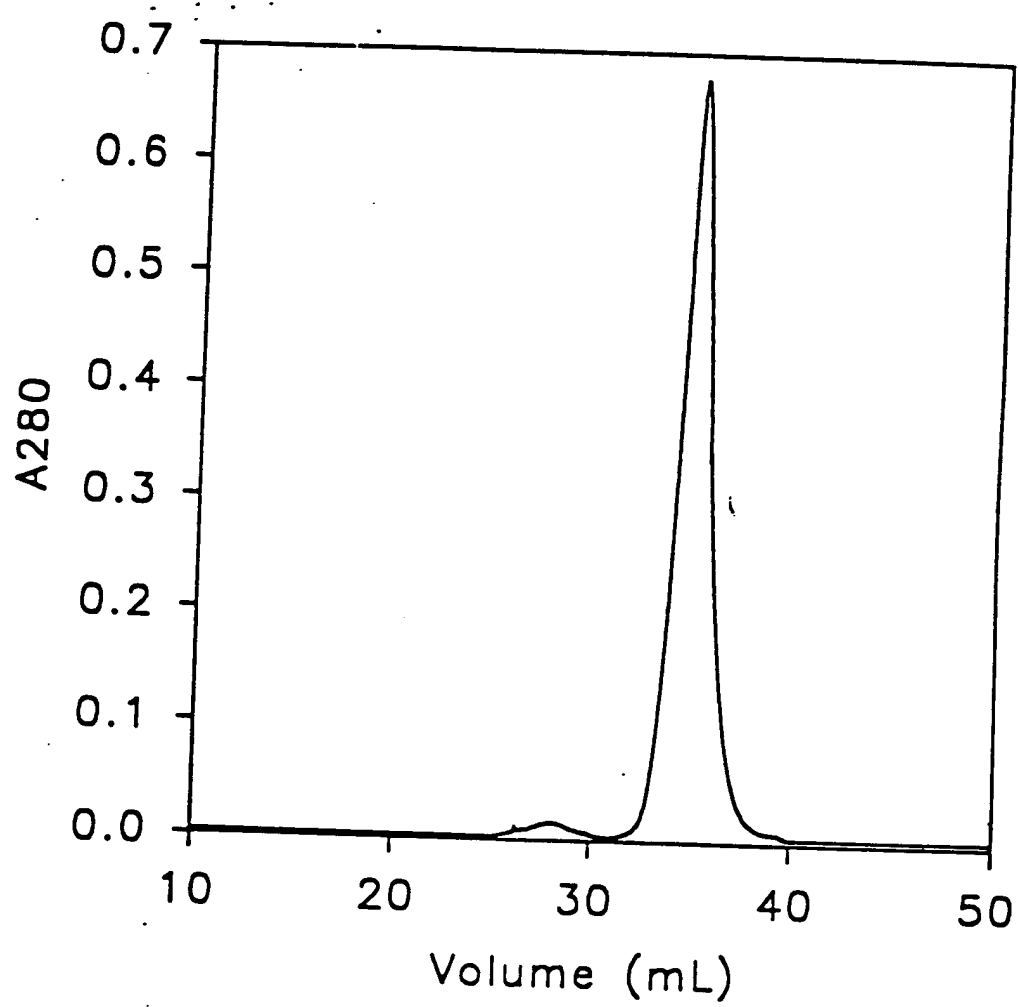
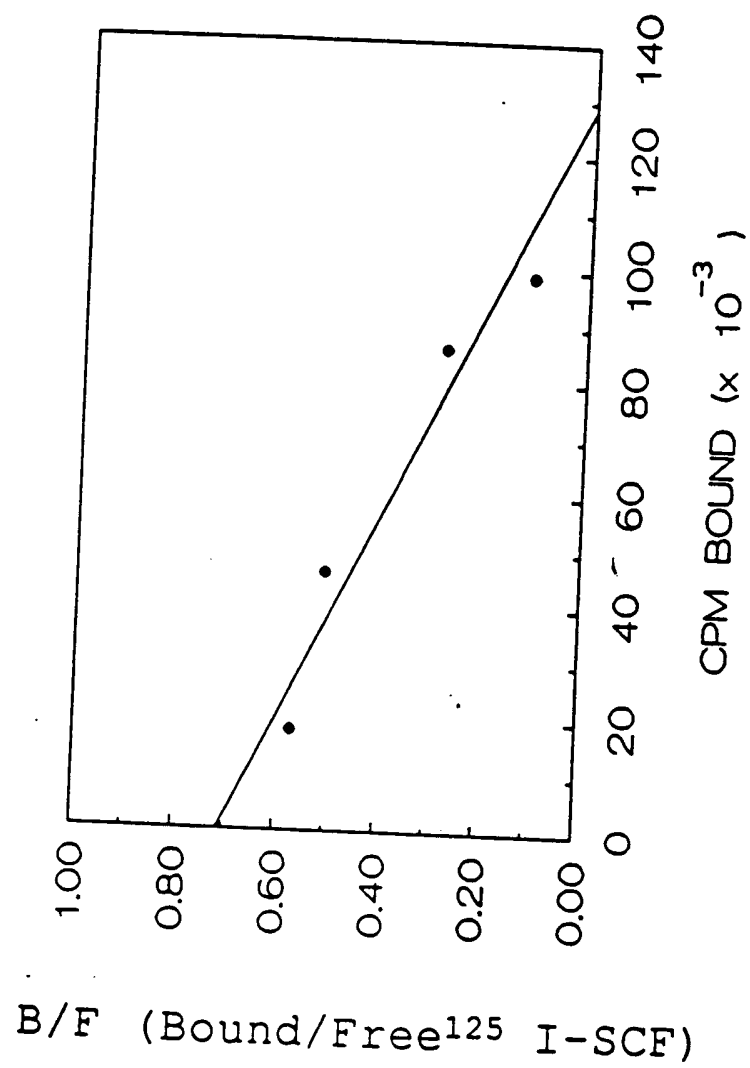


FIG. 41



# FIG. 42A

CCGCCCTCGCGCCGAGACTAGAACGCTGCGGGGAAGCAGGACAGTGGAGAGGGCGCTGCGC 61

TCGGGGCTACCCCAATGCGTGGAATATCTGCCCGCGCTGTTCGTGCAATATGCTGGAGCTCCA 122

GAACAGCTAAACGGAGTCGCCACACCACTGTTTGTGCTGGATCGCAGCGCTGCCCTTTCCCTT 183

-25

-20

Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln  
ATG AAG AAG ACA CAA ACT TGG ATT CTC ACT TGC ATT TAT CTT CAG 228

-10

1

Leu Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg  
CTG CTC CTA TTT AAT CCT CTC GTC AAA ACT GAA GGG ATC TGC AGG 273

10

Asn Arg Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu Val Ala  
AAT CGT GTG ACT AAT AAT GTA AAA GAC GTC ACT AAA TTG GTG GCA 318

20

30

Asn Leu Pro Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly  
AAT CTT CCA AAA GAC TAC ATG ATA ACC CTC AAA TAT GTC CCC GGG 363

40

Met Asp Val Leu Pro Ser His Cys Trp Ile Ser Glu Met Val Val  
ATG GAT GTT TTG CCA AGT CAT TGT TGG ATA AGC GAG ATG GTA GTA 408

50

60

Gln Leu Ser Asp Ser Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn  
CAA TTG TCA GAC AGC TTG ACT GAT CTT CTG GAC AAG TTT TCA AAT 453

# FIG. 42B

Ile Ser Glu Gly Leu Ser Asn Tyr Ser Ile Ile Asp Lys Leu Val	80
ATT TCT GAA GGC TTG AGT AAT TAT TCC ATC ATA GAC AAA CTT GTG	498
Asn Ile Val Asp Asp Leu Val Glu Cys Val Lys Glu Asn Ser Ser	90
AAT ATA GTG GAT GAC CTT GTG GAG TGC GTG AAA GAA AAC TCA TCT	543
Lys Asp Leu Lys Lys Ser Phe Lys Ser Pro Glu Pro Arg Leu Phe	110
AAG GAT CTA AAA AAA TCA TTC AAG AGC CCA GAA CCC AGG CTC TTT	588
Thr Pro Glu Glu Phe Phe Arg Ile Phe Asn Arg Ser Ile Asp Ala	120
ACT CCT GAA GAA TTC TTT TTT AGA ATT TTT AAT AGA TCC ATT GAT GCC	633
Phe Lys Asp Phe Val Val Ala Ser Glu Thr Ser Asp Cys Val Val	140
TTC AAG GAC TTT GTA GTG GCA TCT GAA ACT AGT GAT TGT GTG GTT	678
Ser Ser Thr Leu Ser Pro Glu Lys Asp Ser Arg Val Ser Val Thr	150
TCT TCA ACA TTA AGT CCT GAG AAA GAT TCC AGA GTC AGT GTC ACA	723

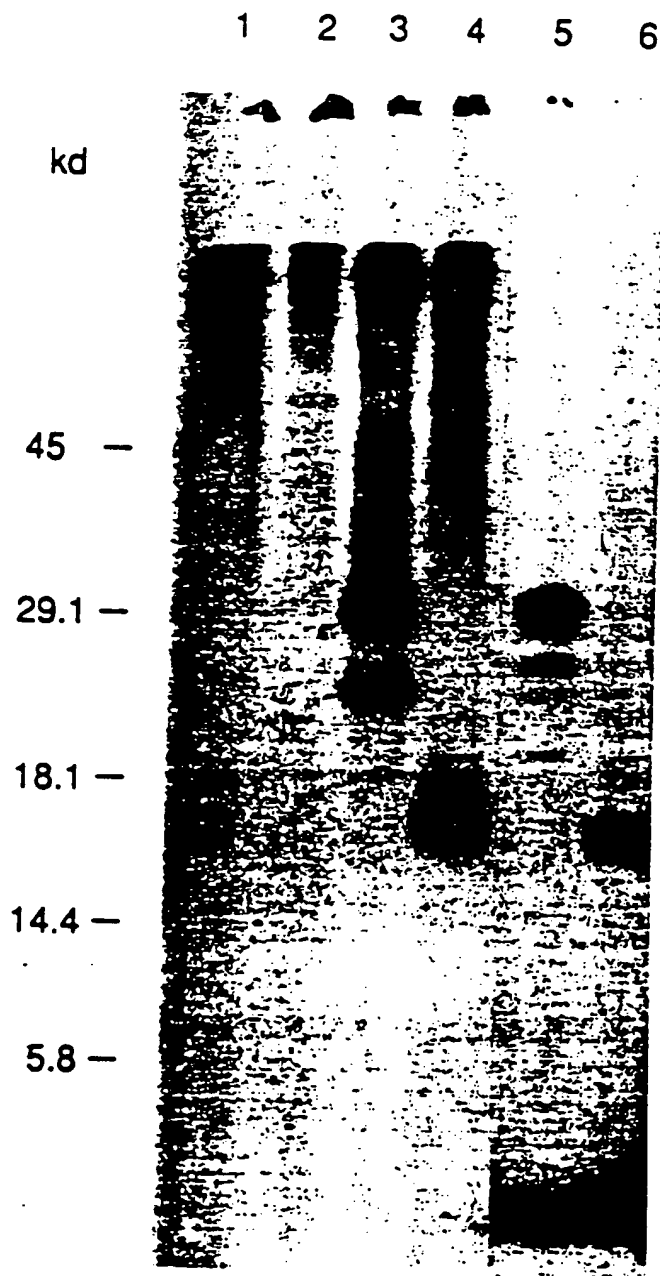
# FIG. 42C

Lys Pro Phe Met Leu Pro Pro Val Ala Ala Ser Ser Leu Arg Asn AAA CCA TTT ATG TTA CCC CCT GTT GCA GCC AGC TCC CTT AGG AAT	160	170	768
Asp Ser Ser Ser Ser Asn Arg Lys Ala Lys Asn Pro Pro Gly Asp GAC AGC AGT AGC AGT AAT AGG AAG GCC AAA AAT CCC CCT GGA GAC	180	813	
Ser Ser Leu His Trp Ala Ala Met Ala Leu Pro Ala Leu Phe Ser TCC AGC CTA CAC TGG GCA GCC ATG GCA TTG CCA GCA TTG TTT TCT	190	200	858
Leu Ile Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys Lys Arg CTT ATA ATT GGC TTT GCT TTT GGA GCC TTA TAC TAC TGG AAG AAG AGA	210	903	
Gln Pro Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile Asn Glu CAG CCA AGT CTT ACA AGG GCA GTT GAA AAT ATA CAA ATT AAT GAA	220	230	948
Glu Asp Asn Glu Ile Ser Met Leu Gln Glu Lys Glu Arg Glu Phe GAG GAT AAT GAG ATA AGT ATG TTG CAA GAG AAA GAG AGA GAG TTT	240	993	
Gln Glu Val End CAA GAA GTG TAA	248		
TTGTGGCTTGATCAACACTGTTACTTTCGTACATTGGC 1044			

## FIG. 42D

TGGTAACAGTTCAATGTTTGCTTCATAAATGAAGCAGCCTTTAAACAAATTCATATCTCTGTC 1104  
TGGAGTGACAGACCATCTTTATCTGTTCTTGCTACCCATGACTTTATATGGATGATTC 1164  
AGAAATTGGAAACAGAAATGTTTACTGTGAAACTGGCACTGAATTAATCATCTATAAAGAA 1224  
GAACTTGCAATGGAGCAGGACTCTATTTTAAGGACTGCCGGGACTTGGGTCTCATTTAGAAC 1284  
TTGCAGCTGATGTTGGAAGAGAAAGCACGTGTCTCAGACTGCATGTACCATTTCATGGC 1344  
TCCAGAAATGTCTAAATGCTGAAAAAACACCTAGCTTTATTCTTCAGATACAAACTGCAG 1404

FIG. 43





# FIG. 44A

	AGCAGGGACAGTGGAGAGGGCGCTGCGCTC	30
GGGCTACCCAATGCGTGGACTATCTGCCCGCGCTGTTCTGTGCAATATGCTGGAGCTCCAG		90
AACAGCTAAACGGAGTCGCCACACCACTGTTTGTGTGGATCGCAGCGCTGCCCTTTCCTT		150
-25		
	-20	
Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln		
ATG AAG AAG ACA CAA ACT TGG ATT CTC ACT TGC ATT TAT CTT CAG		195
-10		
Leu Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg	1	
CTG CTC CTA TTT AAT CCT CTC GTC AAA ACT GAA GGG ATC TGC AGG		240
	10	
Asn Arg Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu Val Ala	20	
AAT CGT GTG ACT AAT AAT GTA AAA GAC GTC ACT AAA TTG GTG GCA		285
	30	
Asn Leu Pro Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly		
AAT CTT CCA AAA GAC TAC ATG ATA ACC CTC AAA TAT GTC CCC GGG		330
	40	
Met Asp Val Leu Pro Ser His Cys Trp Ile Ser Glu Met Val Val	50	
ATG GAT GTT TTG CCA AGT CAT TGT TGG ATA AGC GAG ATG GTA GTA		375

Gln	Leu	Ser	Asp	Ser	Leu	Thr	Asp	Leu	Leu	Asp	Lys	Phe	Ser	Asn	420
CAA	TTG	TCA	GAC	AGC	TTG	ACT	GAT	CTT	CTG	GAC	AAG	TTT	TCA	AAT	
															60
Ile	Ser	Glu	Gly	Leu	Ser	Asn	Tyr	Ser	Ile	Ile	Asp	Lys	Leu	Val	80
ATT	TCT	GAA	GGC	TTG	AGT	AAT	TAT	TCC	ATC	ATA	GAC	AAA	CTT	GTG	
															465
Asn	Ile	Val	Asp	Asp	Leu	Val	Glu	Cys	Val	Lys	Glu	Asn	Ser	Ser	510
AAT	ATA	GTG	GAT	GAC	CTT	GTG	GAG	TGC	GTG	AAA	GAA	AAC	TCA	TCT	
															100
Lys	Asp	Leu	Lys	Lys	Ser	Phe	Lys	Ser	Pro	Glu	Pro	Arg	Leu	Phe	110
AAG	GAT	CTA	AAA	AAA	TCA	TTC	AAG	AGC	CCA	GAA	CCC	AGG	CTC	TTT	
															555
Thr	Pro	Glu	Glu	Phe	Phe	Arg	Ile	Phe	Asn	Arg	Ser	Ile	Asp	Ala	600
ACT	CCT	GAA	GAA	TTC	TTT	AGA	ATT	TTT	AAT	AGA	TCC	ATT	GAT	GCC	
															120
Phe	Lys	Asp	Phe	Val	Val	Ala	Ser	Glu	Thr	Ser	Asp	Cys	Val	Val	140
TTC	AAG	GAC	TTT	GTA	GTG	GCA	TCT	GAA	ACT	AGT	GAT	TGT	GTG	GTT	
															130
Ser	Ser	Thr	Leu	Ser	Pro	Glu	Lys	Gly	Lys	Ala	Lys	Asn	Pro	Pro	645
TCT	TCA	ACA	TTA	AGT	CCT	GAG	AAA	GGG	AAG	GCC	AAA	AAT	CCC	CCT	
															150
															690

# FIG. 44C

```

160      Gly Asp Ser Ser Leu His Trp Ala Ala Met Ala Leu Pro Ala Leu      170
      GGA GAC TCC AGC CTA CAC CAC TGG GCA GCC ATG GCA TTG CCA GCA TTG      735

180      Phe Ser Leu Ile Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys
      TTT TCT CTT ATA ATT GGC TTT GCT TTT GGA GCC TTA TAC TGG AAG      780

190      Lys Arg Gln Pro Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile      200
      AAG AGA CAG CCA AGT CTT ACA AGG GCA GTT GAA AAT ATA CAA ATT      825

210      Asn Glu Glu Asp Asn Glu Ile Ser Met Leu Gln Glu Lys Glu Arg
      AAT GAA GAG GAT AAT GAG ATA AGT ATG TTG CAA GAG AAA GAG AGA      870

220      Glu Phe Gln Glu Val End
      GAG TTT CAA GAA GTG TAA      TTGTGGCTGTATCAACACTGTTACTTTCGTA      920
      CATGGCTGGTAACAGTTCATGTTTGCTTCATAAATGAAGCAGCTTTAAACAATTCATA      980
      TTCTGTCTGGAGTGACAGACCACATCTTTATCTGTCTTGCTACCCATGACTTTATATGG      1040
      ATGATTCAGAAATTGGAACAGAAATGTTTTACTGTGAAACTGGCACTGA      1088

```

FIG. 45

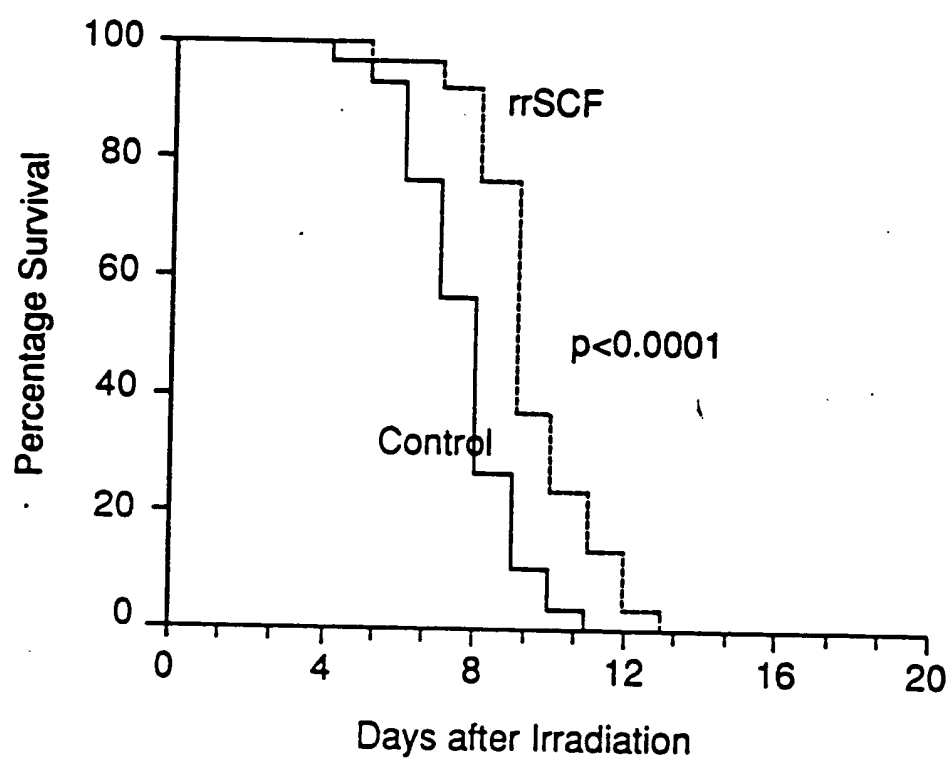
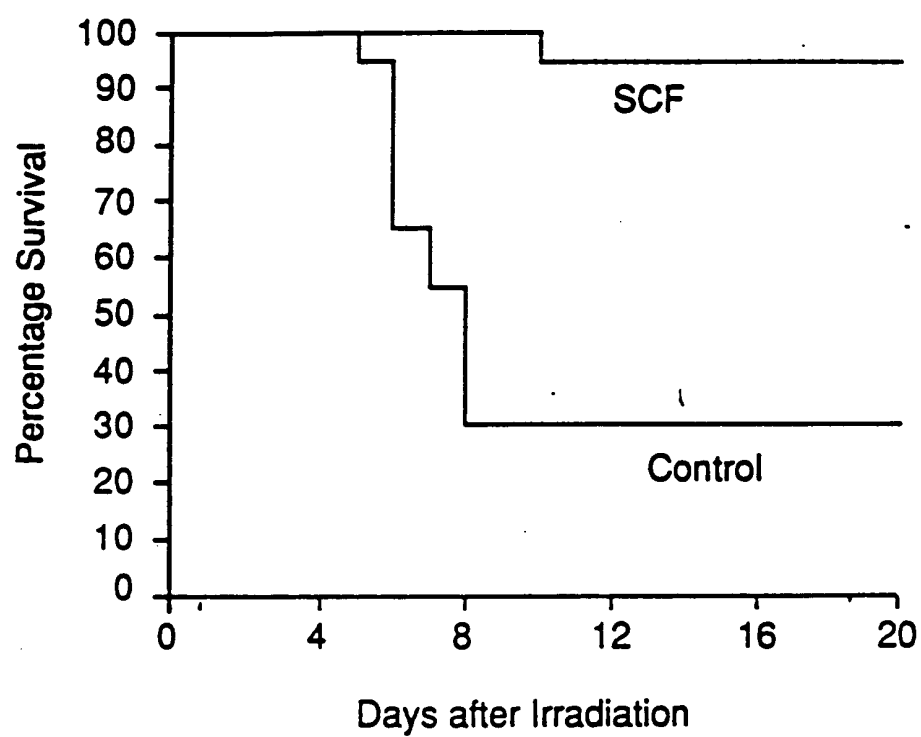


FIG. 46



850 RADS; 5% of femur transplanted

FIG. 47

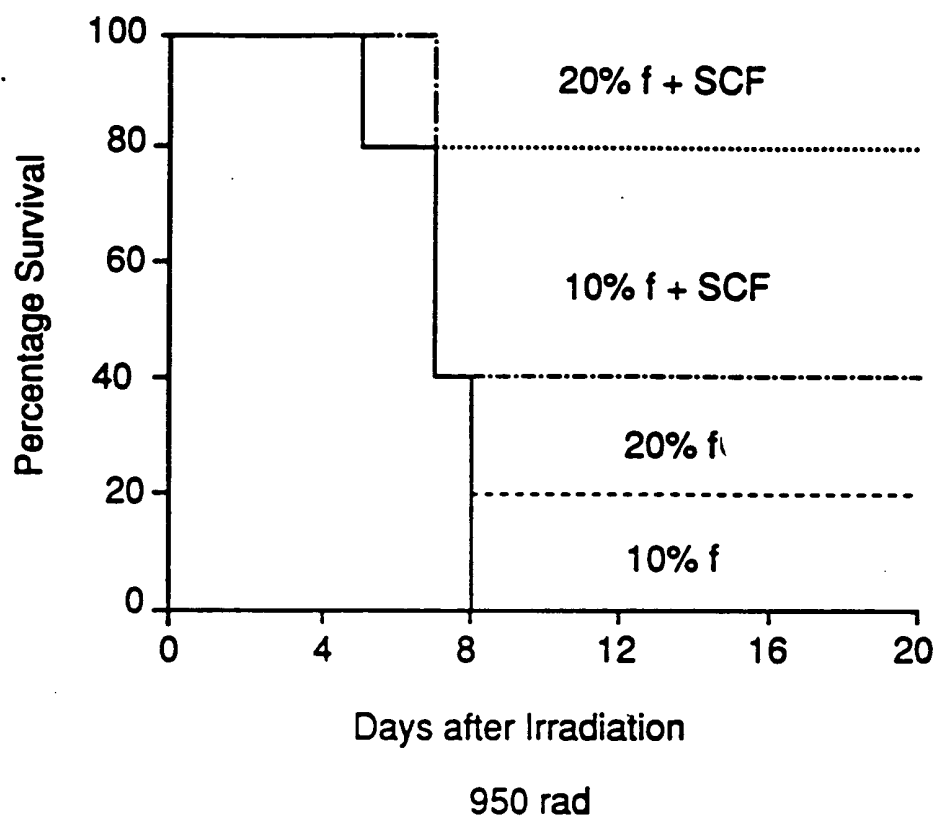


FIG. 48

## SCF RADIOPROTECTION (1163 RAD)

Normal Female BDF1 mice, n=30

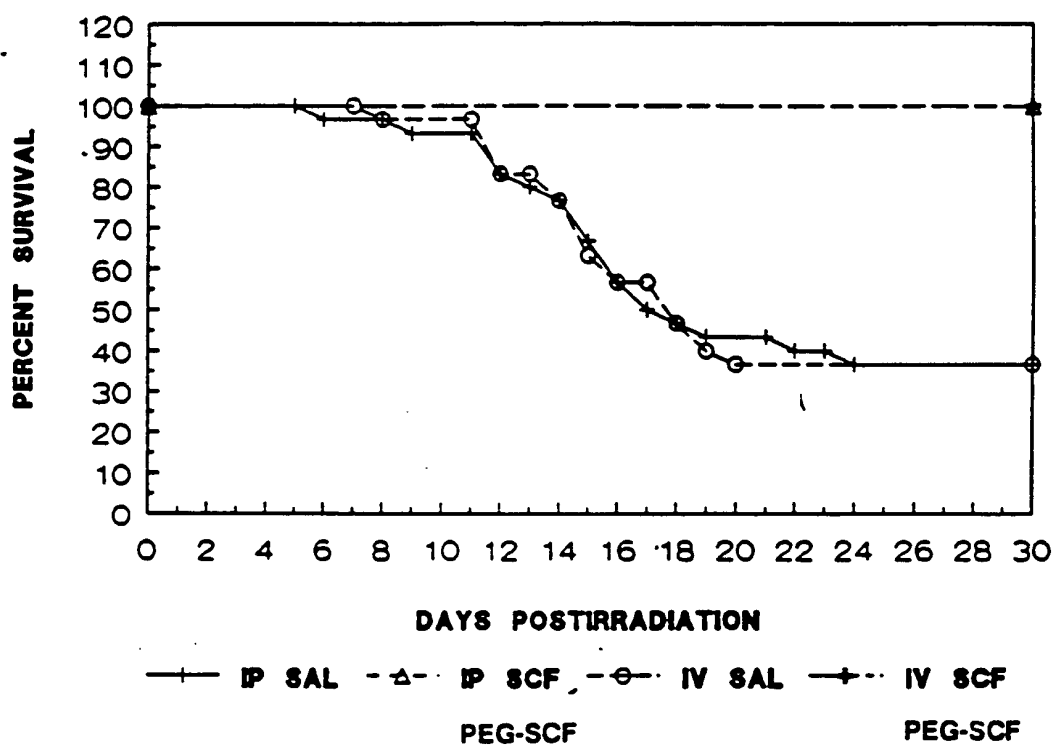


FIG. 49

**SCF RADIOPROTECTION (1159 RAD)**

Normal Female BDF1 mice

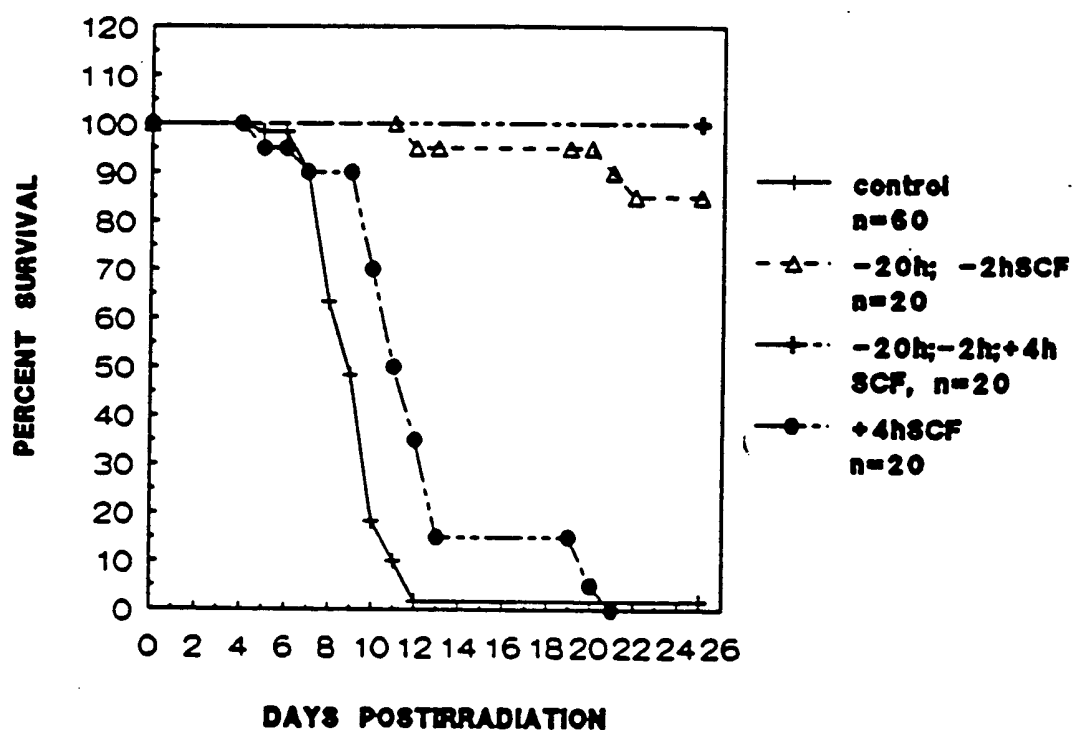




FIG. 50

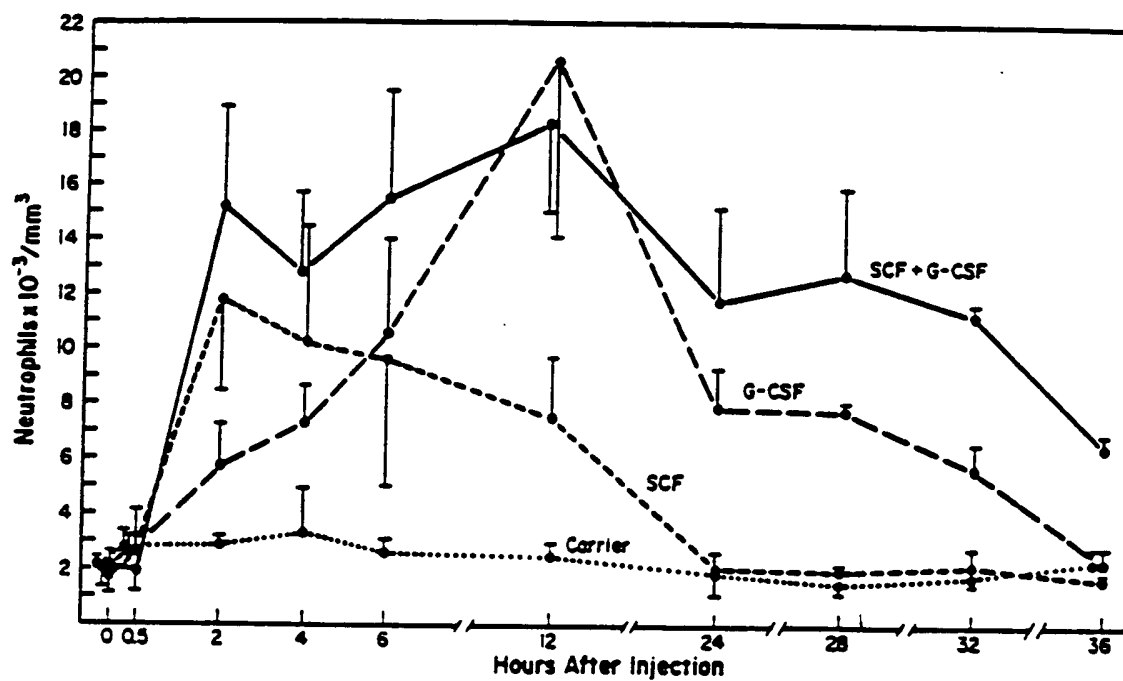


FIG. 51

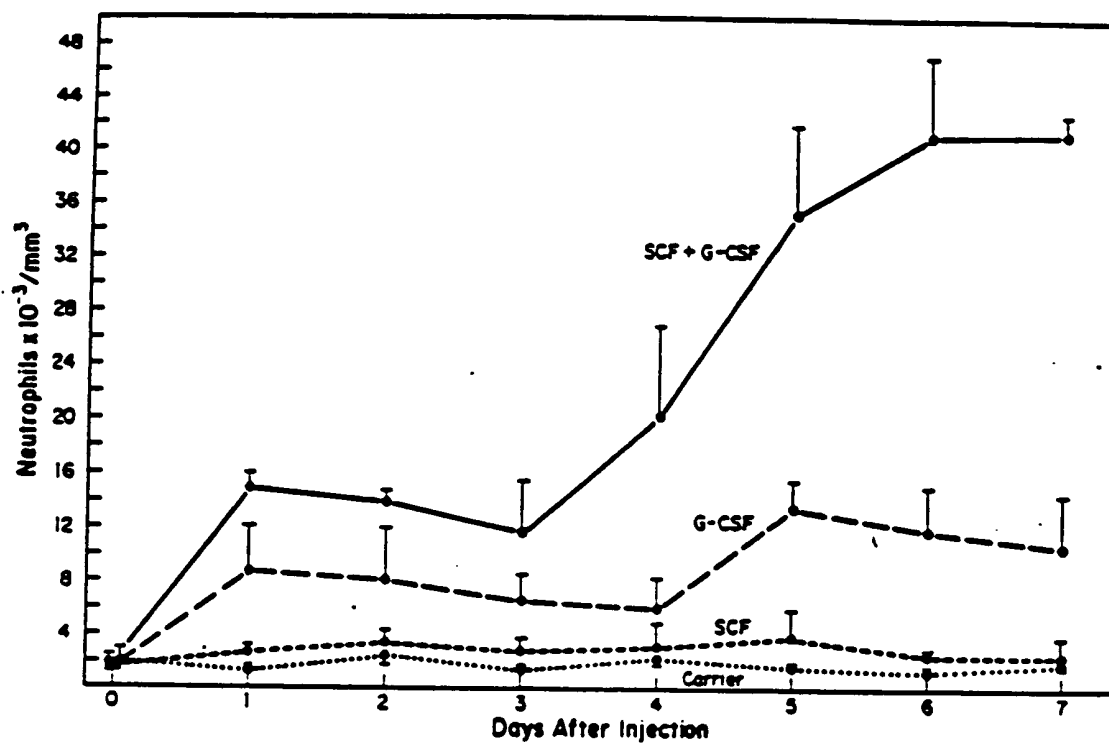


FIG. 52

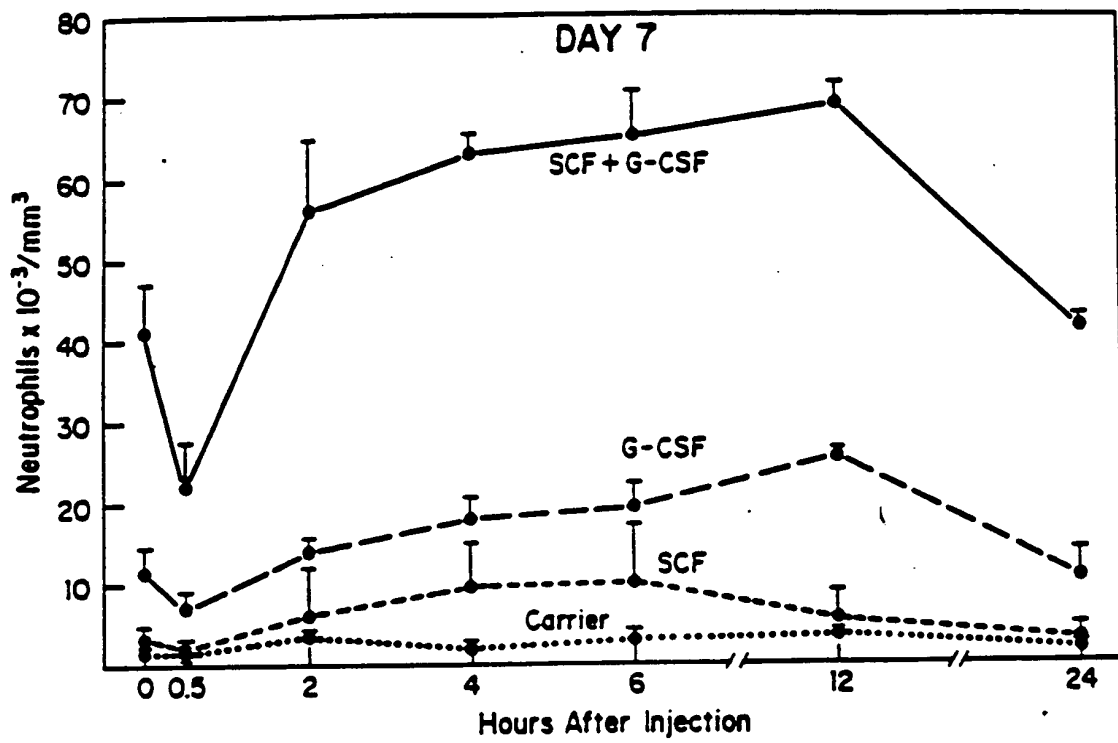


FIG. 53

in vivo Administration of SCF--Platelet Counts

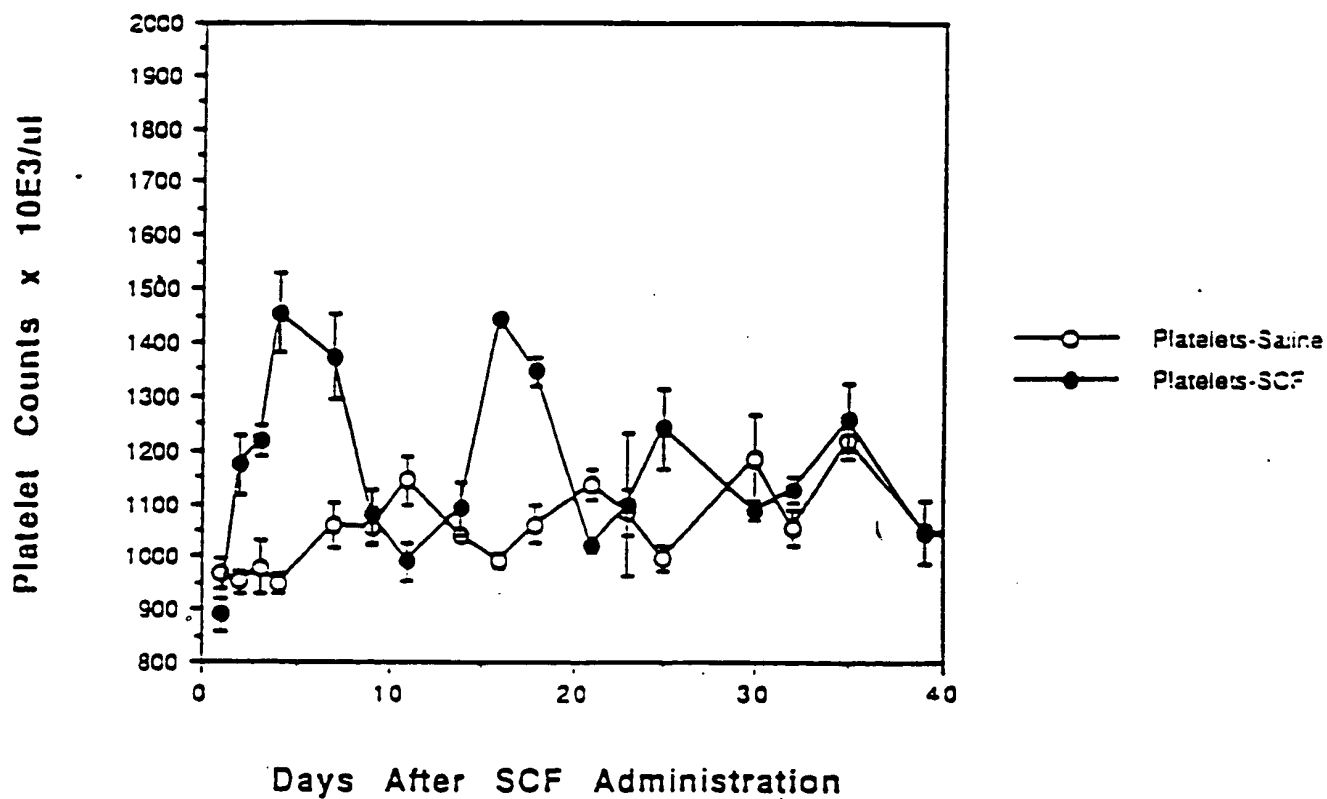


FIG. 54

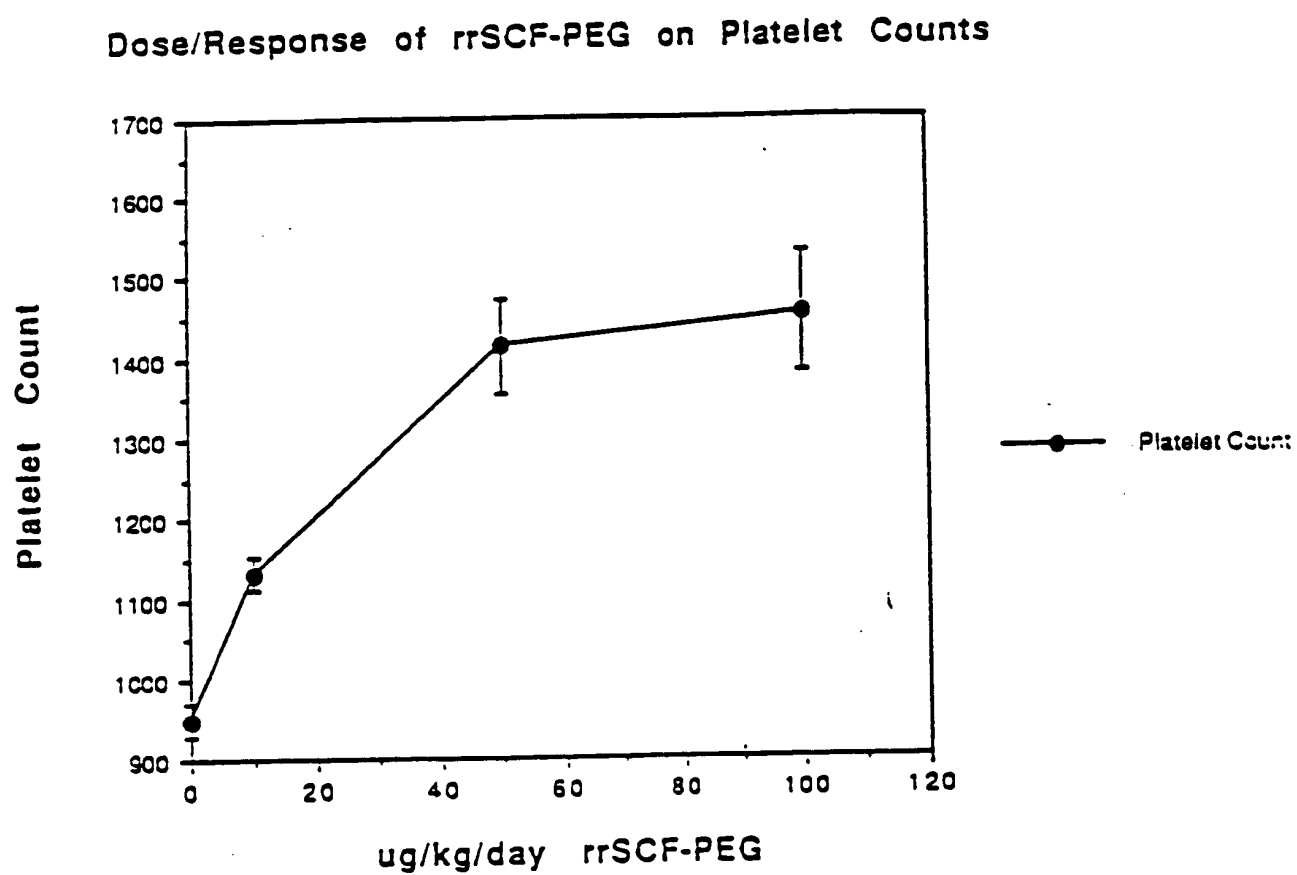


FIG. 55

Effect of 5-FU on platelet levels

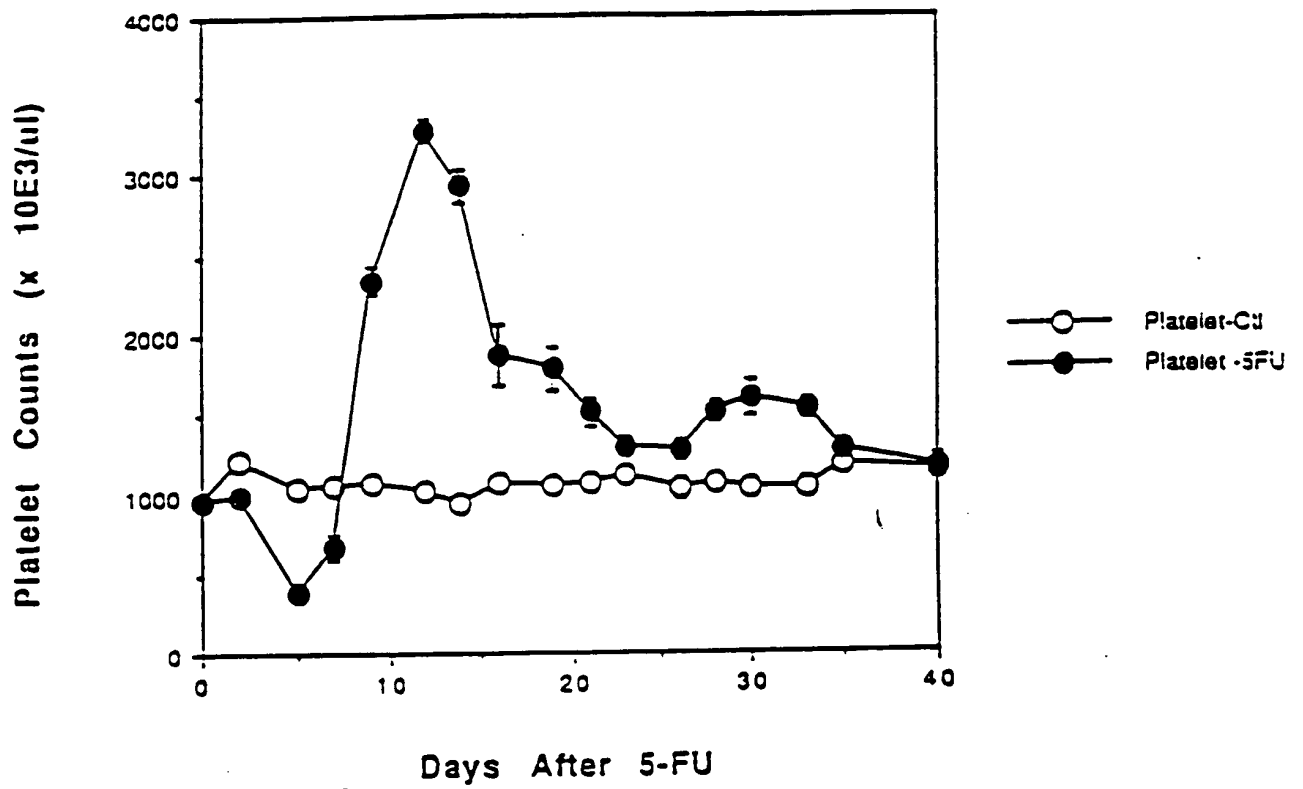
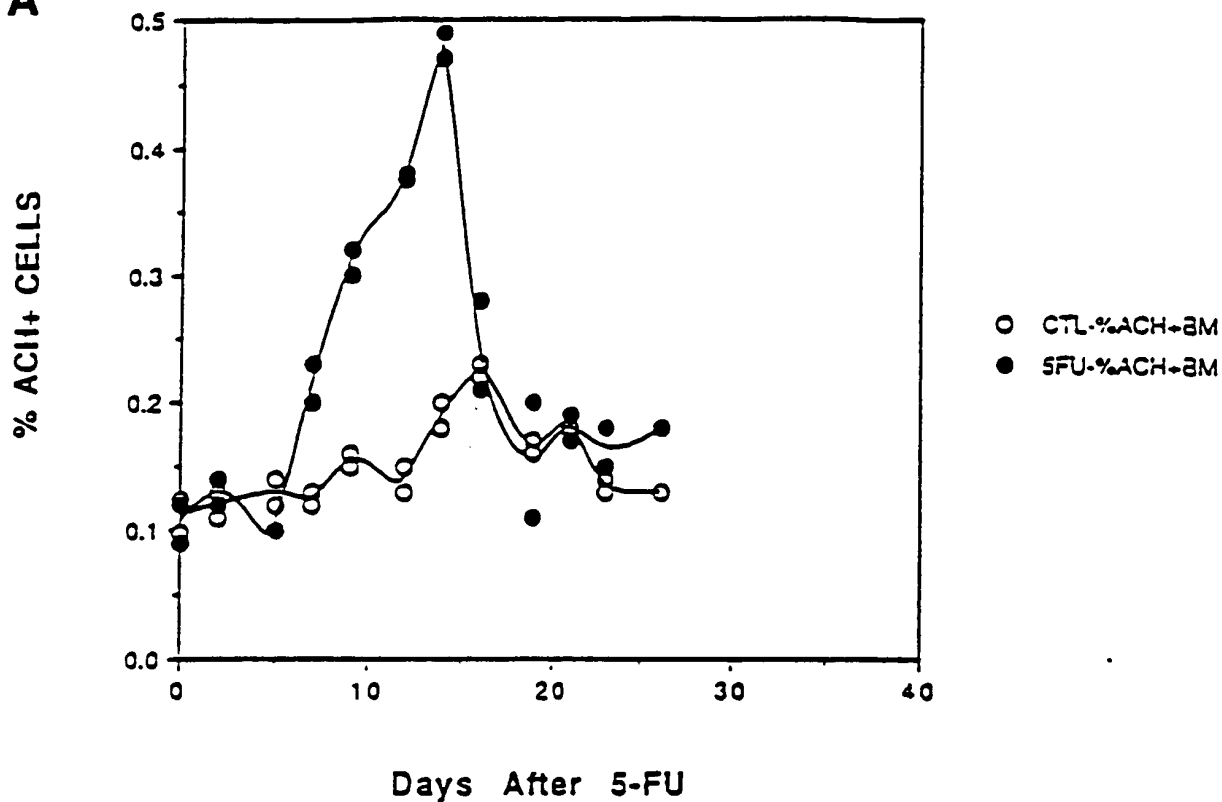


FIG. 56

5-FU Effect on ACH+ Cells in Marrow

A



5-FU Effect on ACH+ Cells in Spleen

B

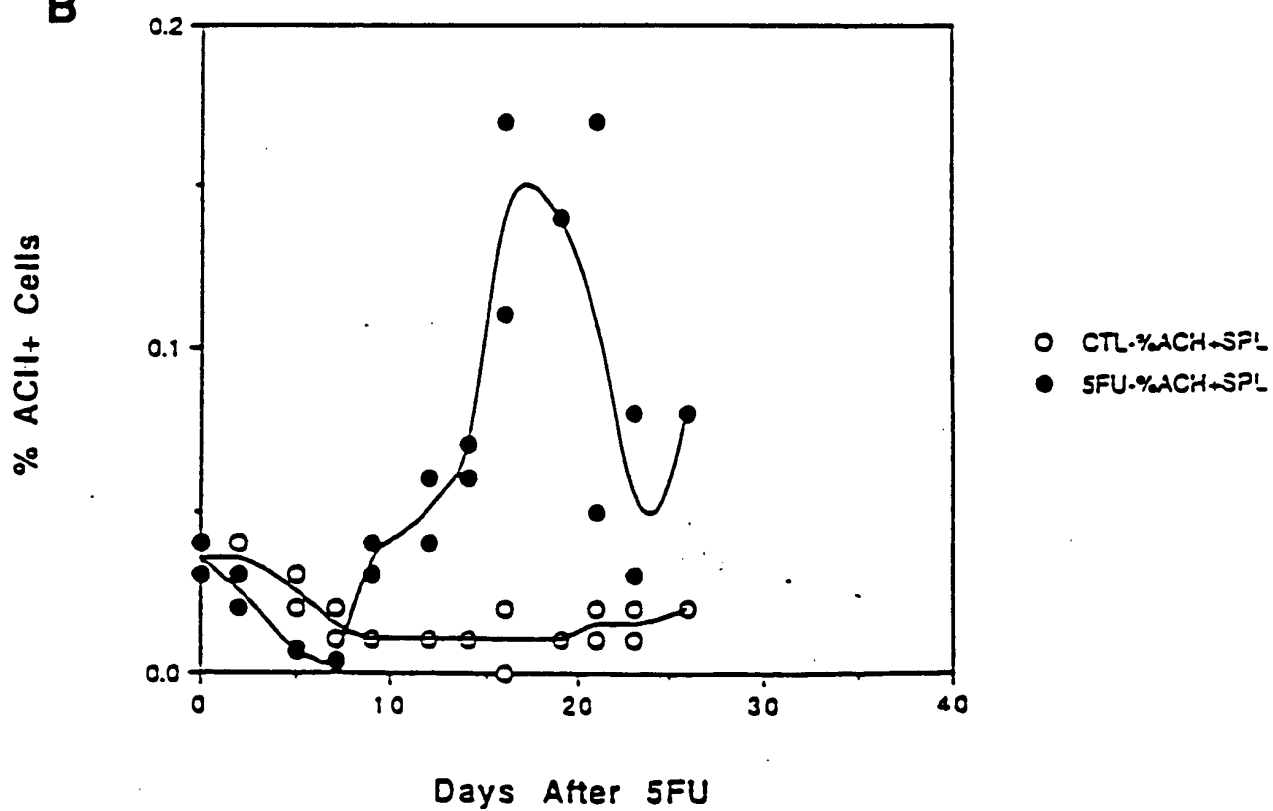


FIG. 57

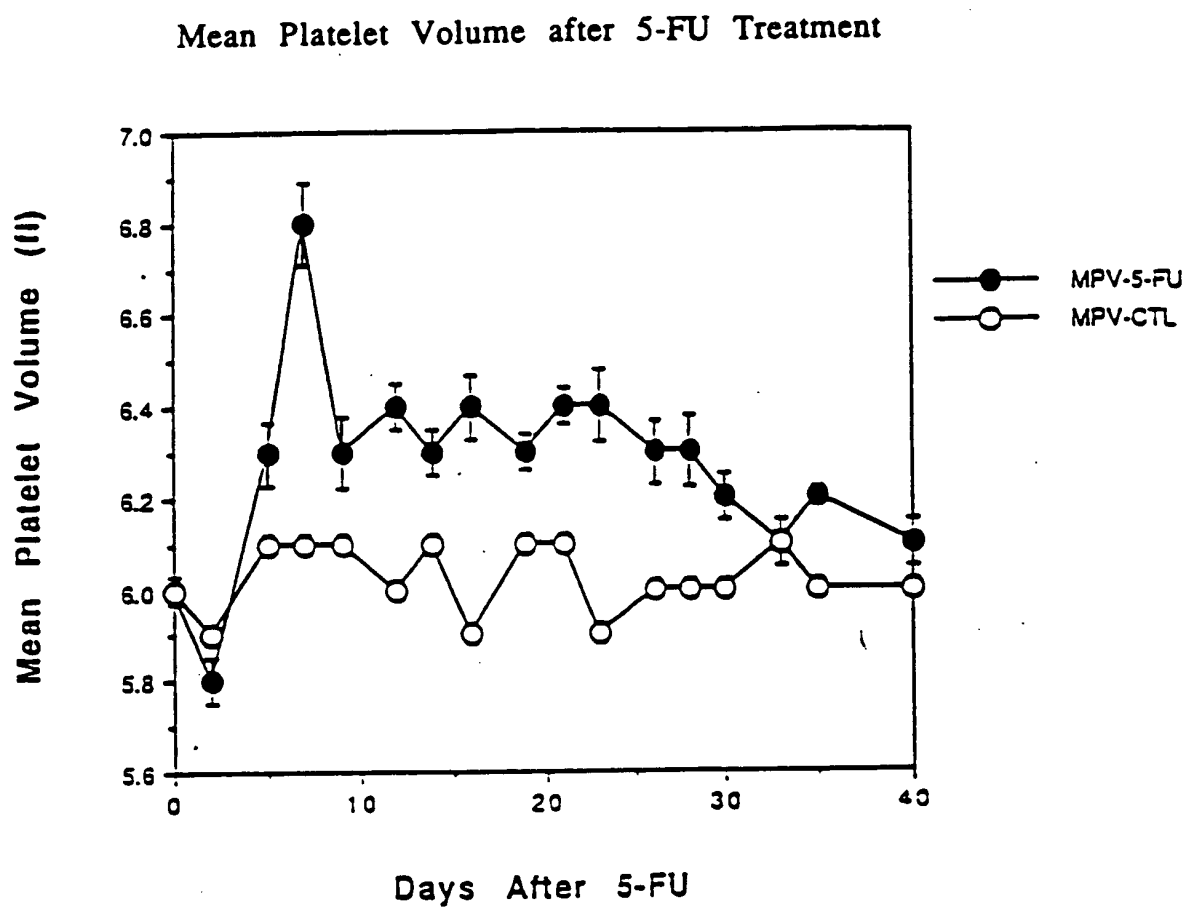




FIG. 58

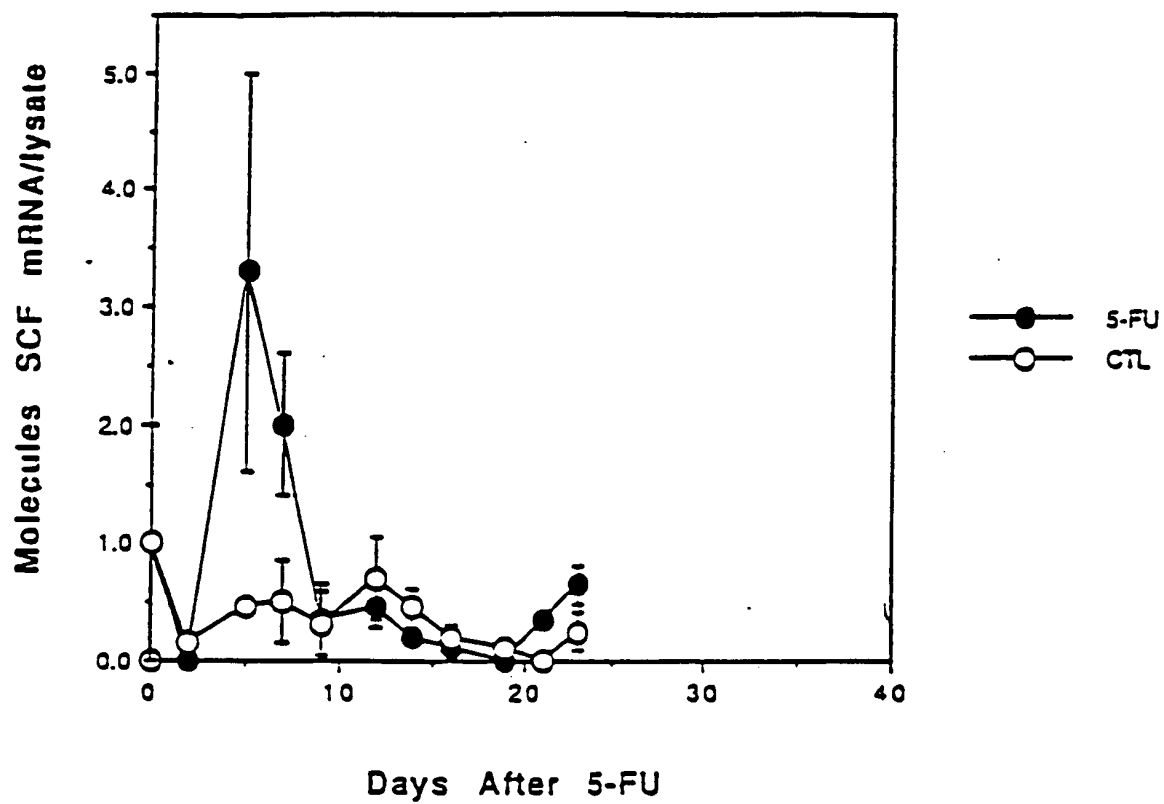


FIG. 59

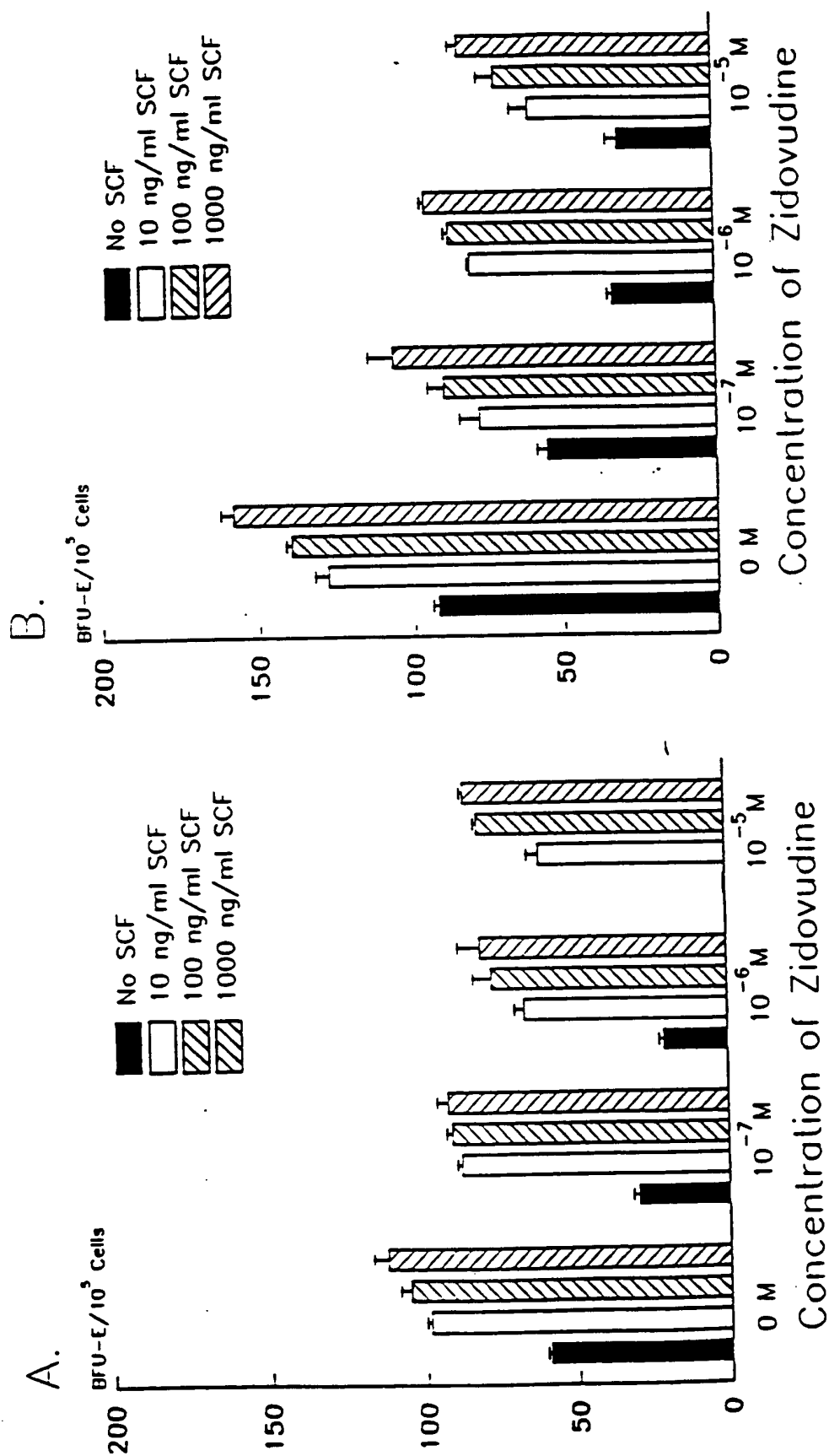


FIG. 60

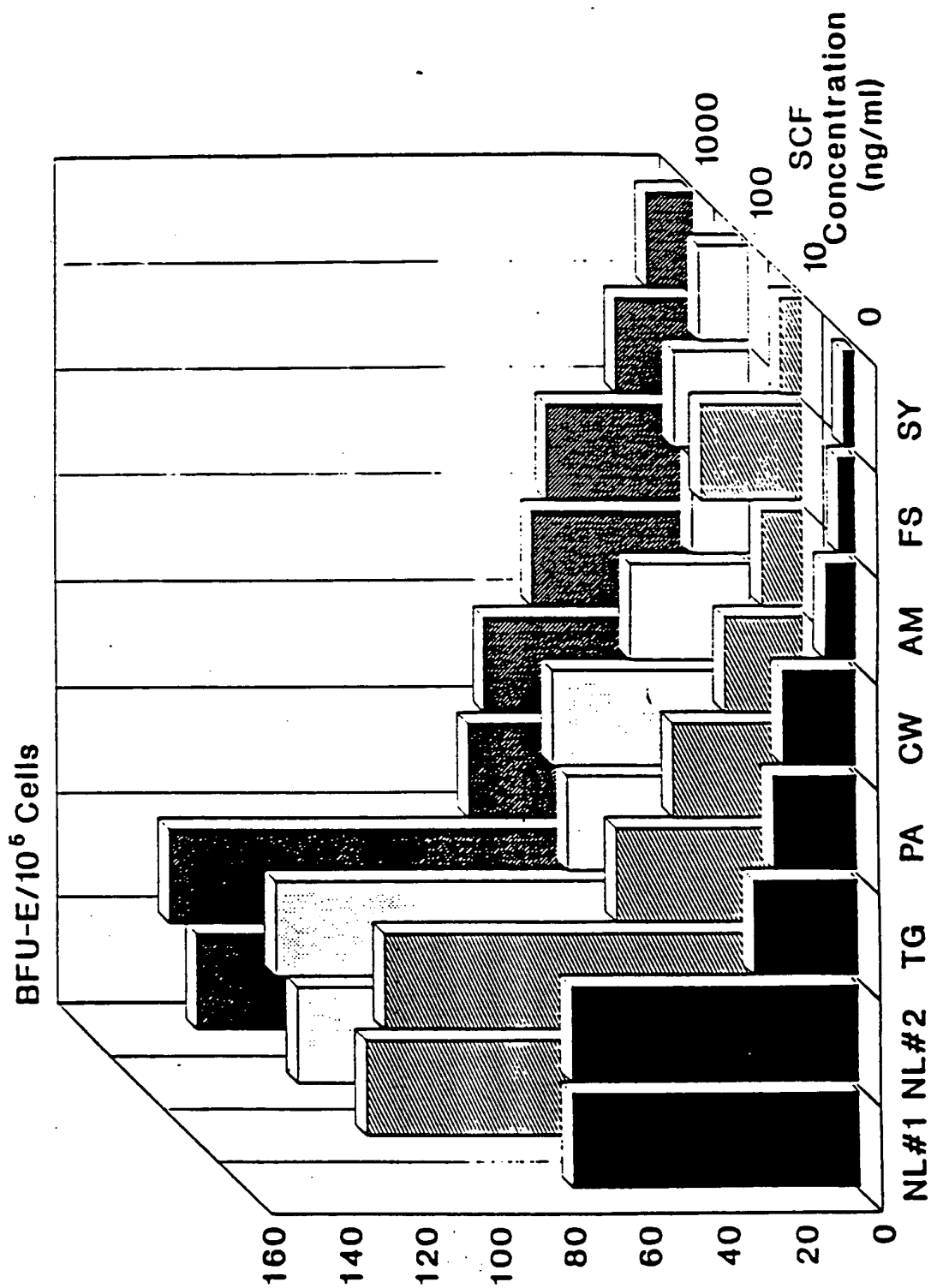


FIG: 61

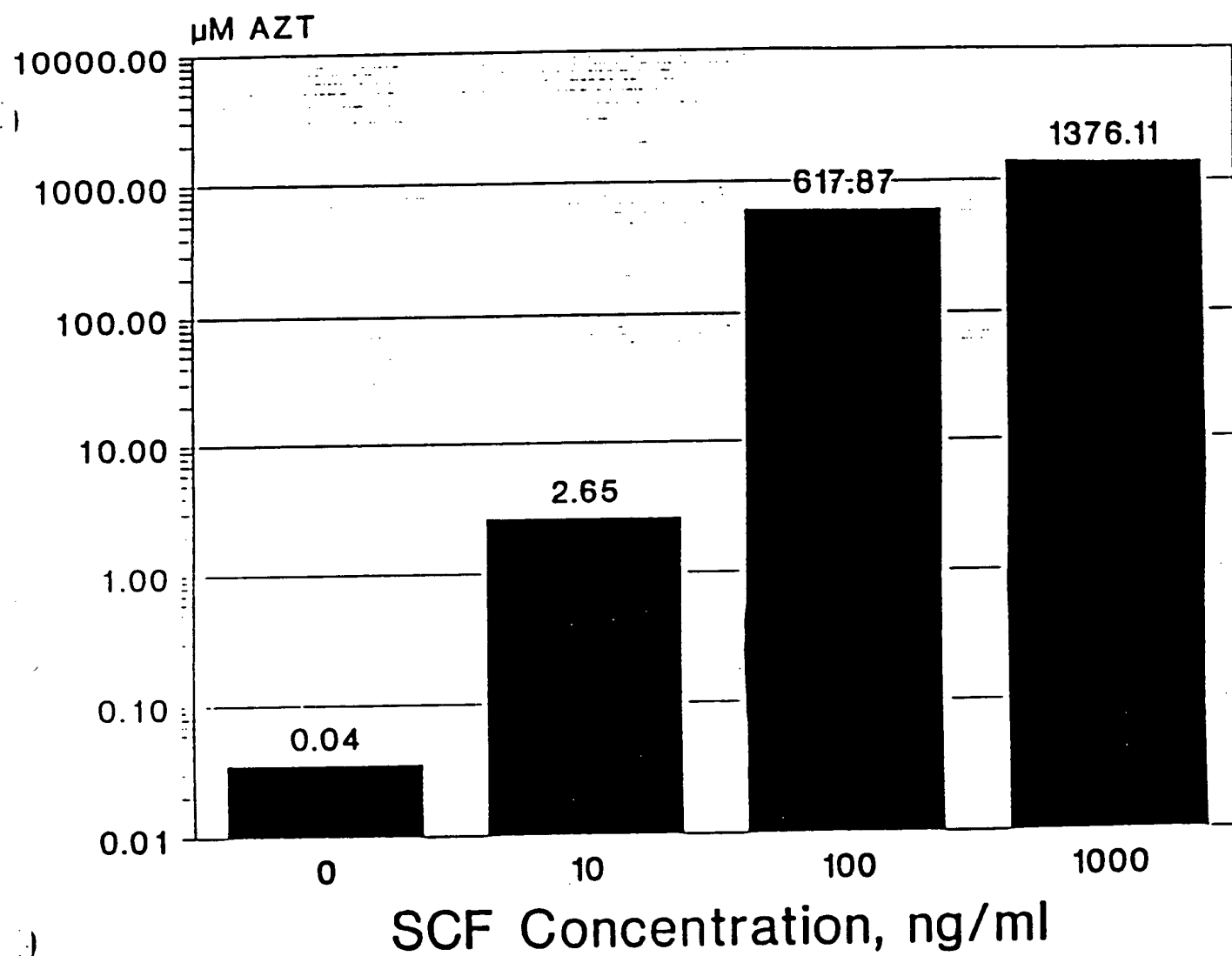


FIG. 62

# EFFECT OF SCF ON AZT SUPPRESSION OF BMC

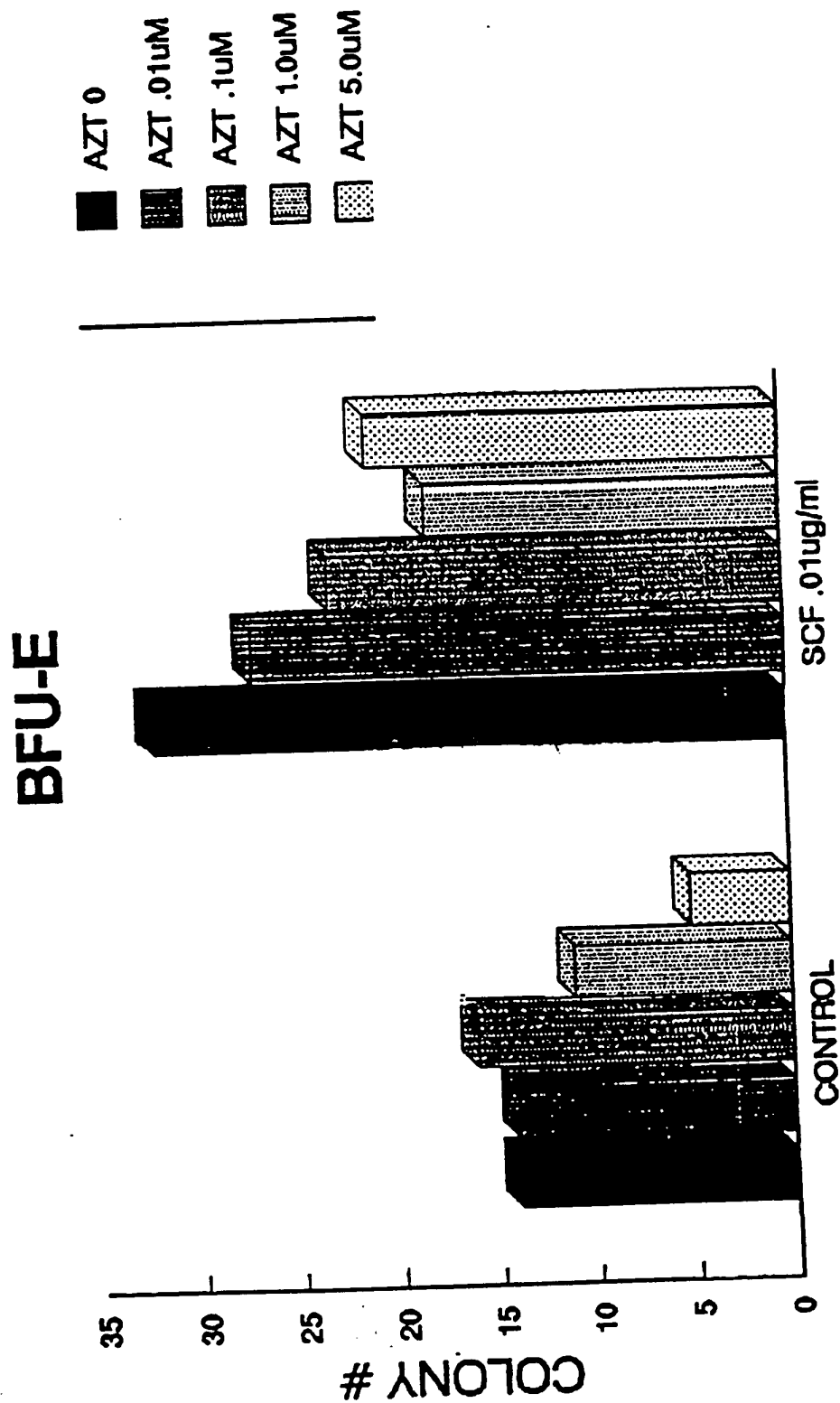


FIG. 63

# EFFECT OF SCF ON AZT SUPPRESSION OF BMC

CFU-GM

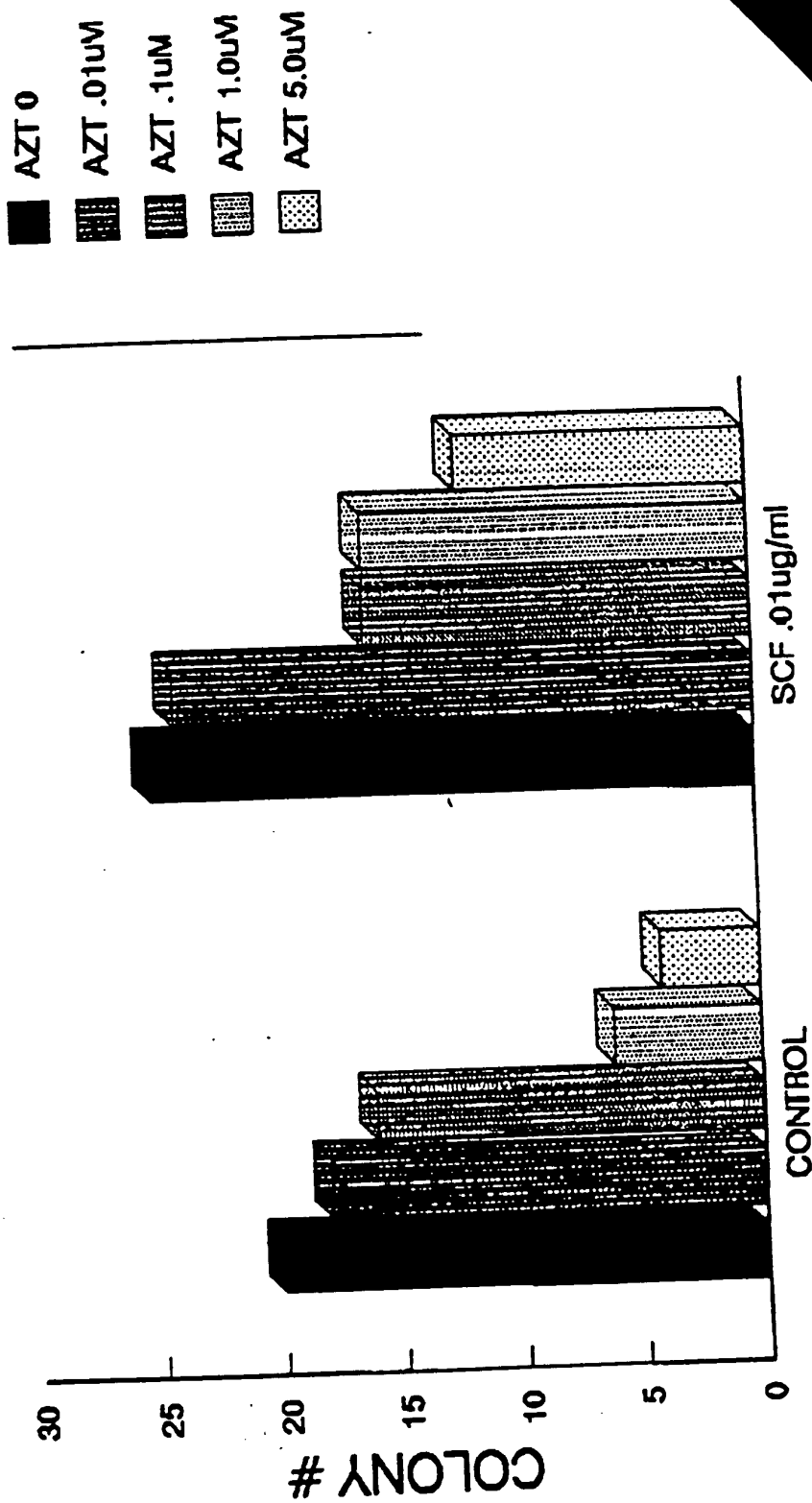


FIG. 64

# EFFECT OF SCF ON GANCICLOVIR SUPPRESSION OF BMC

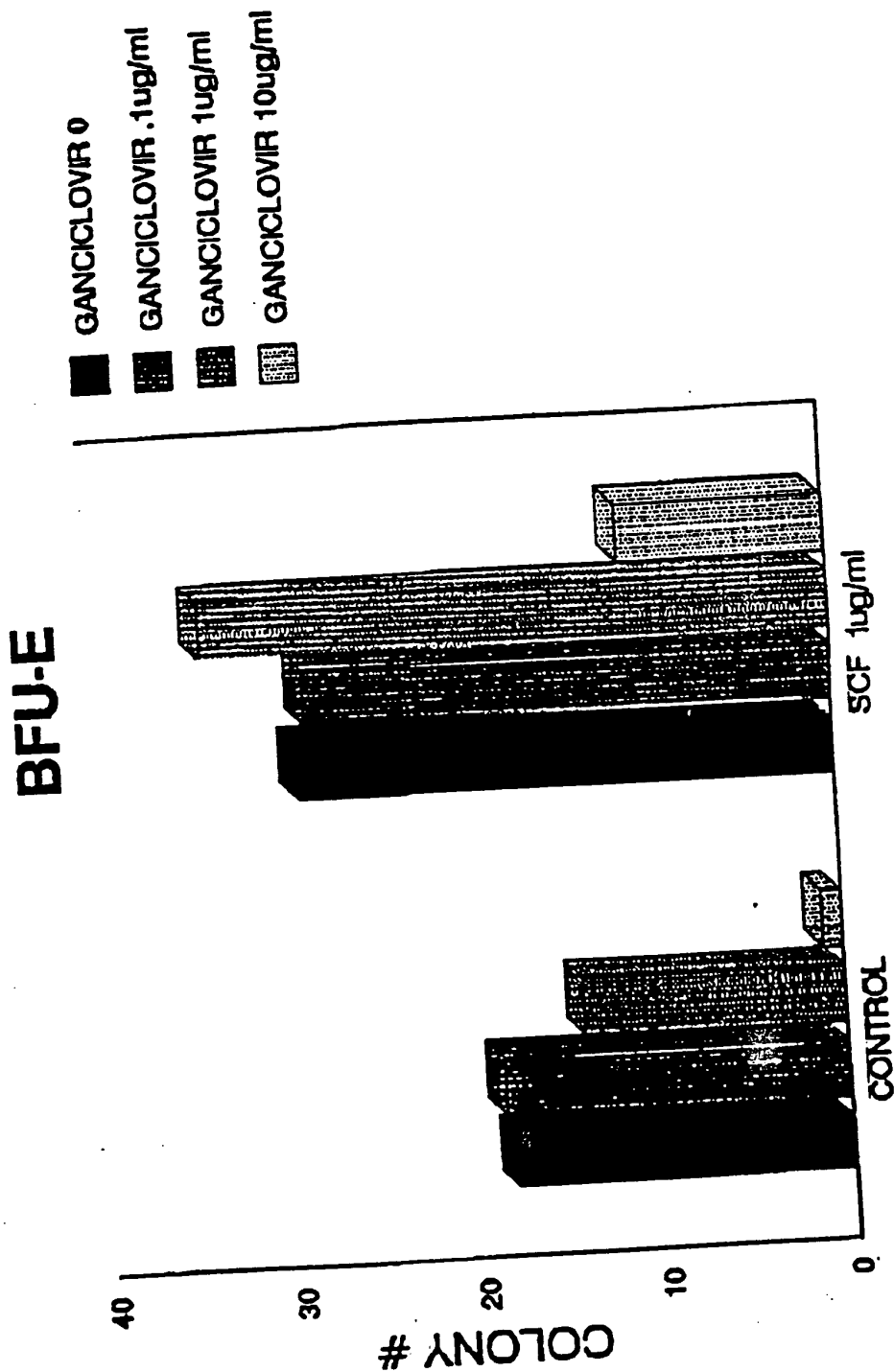


FIG. 65

# EFFECT OF SCF ON GANCICLOVIR SUPPRESSION OF BMC

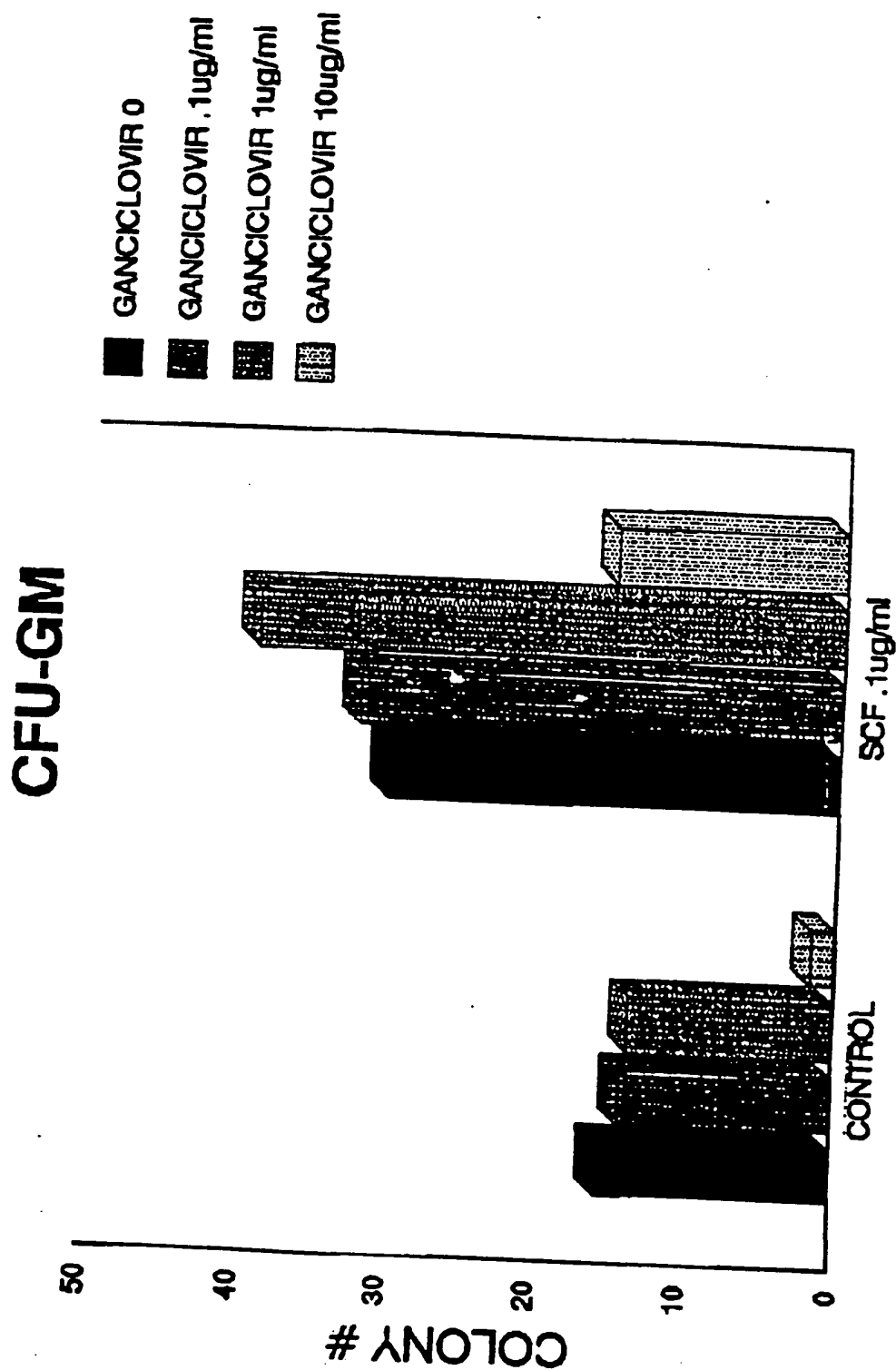




FIG. 66

Effects of SCF on CFU-S Number

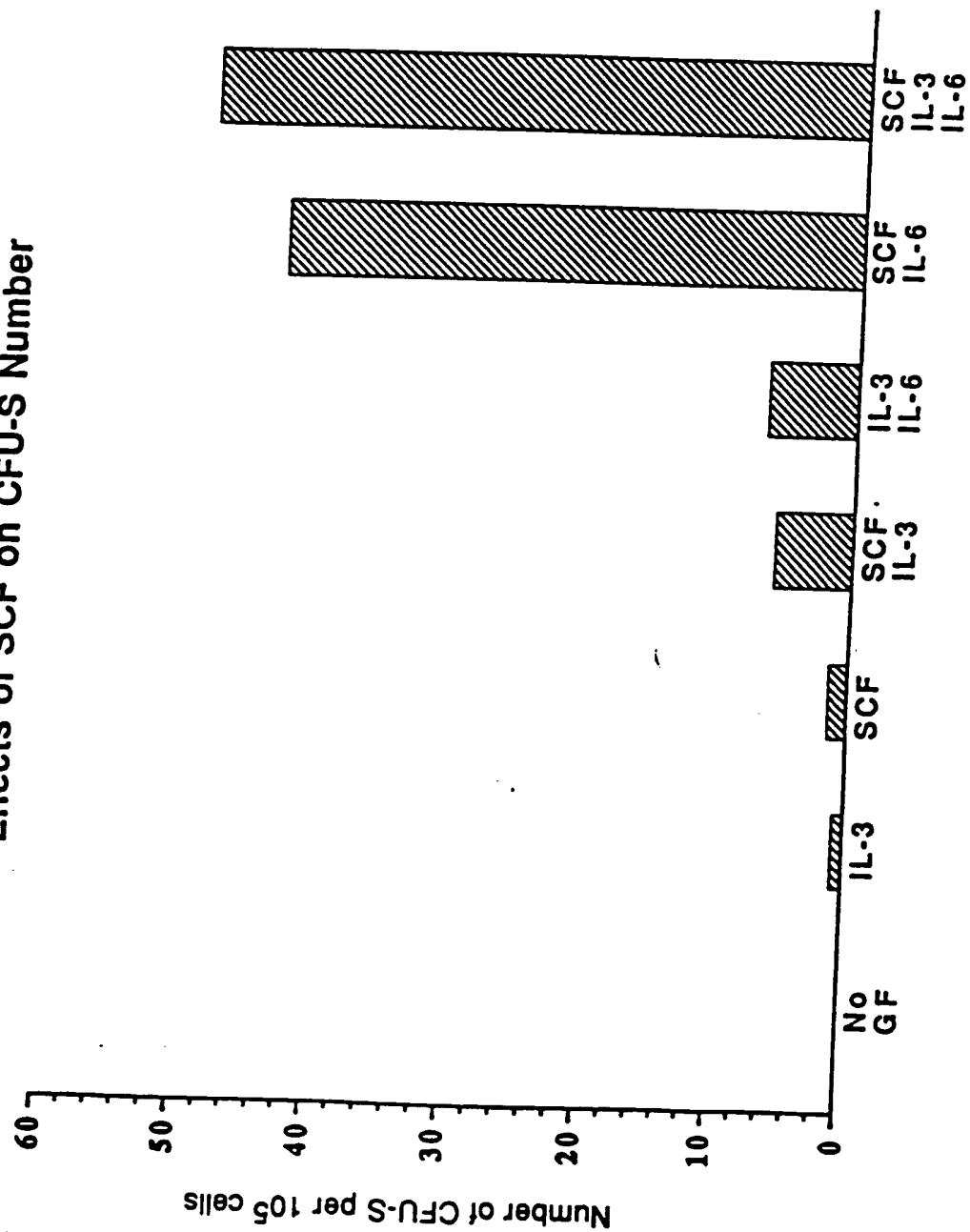


FIG. 67

EFFECTS OF SCF ON SHORT TERM REPOPULATING ABILITY (35 DAYS)

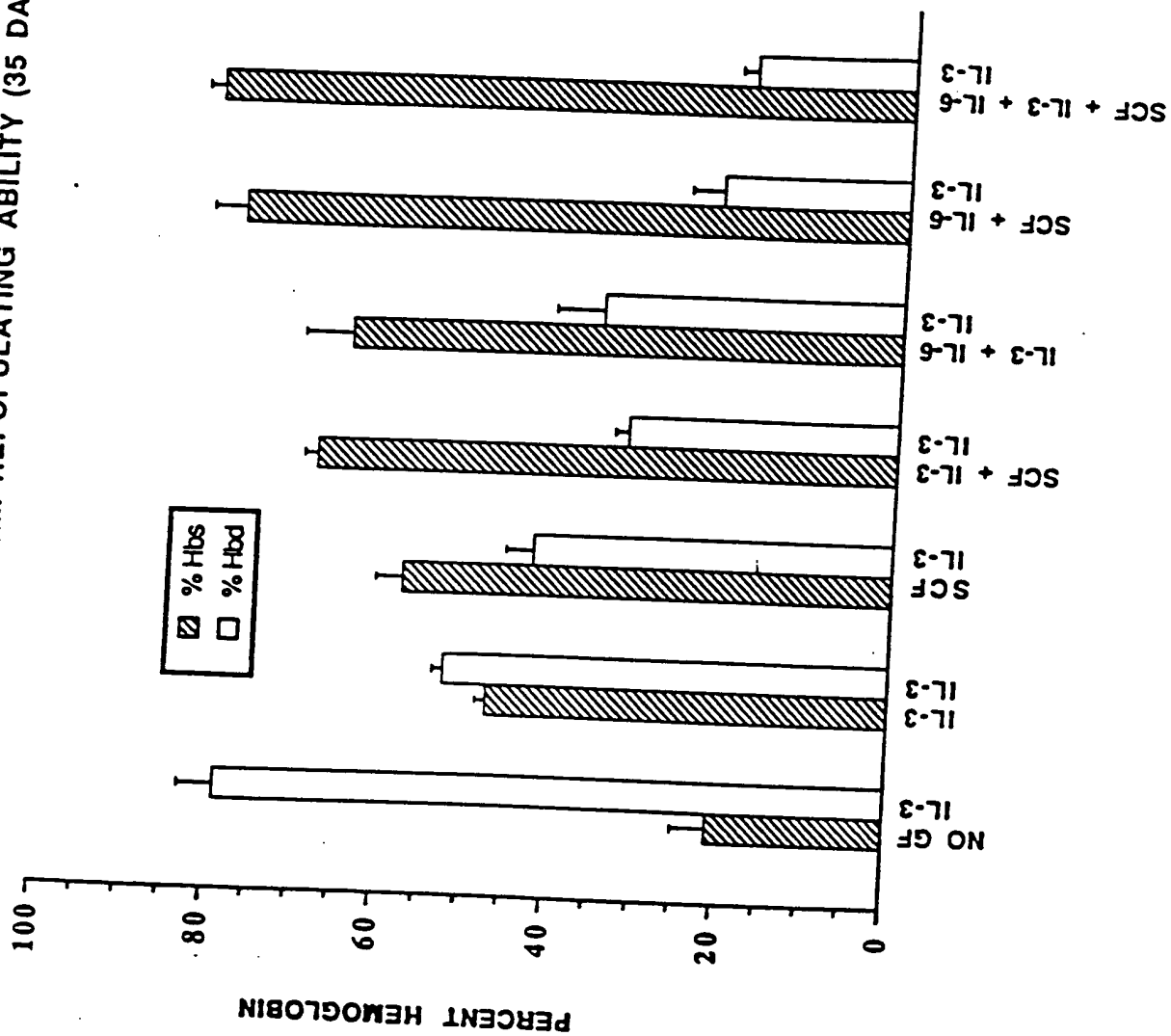


FIG. 68

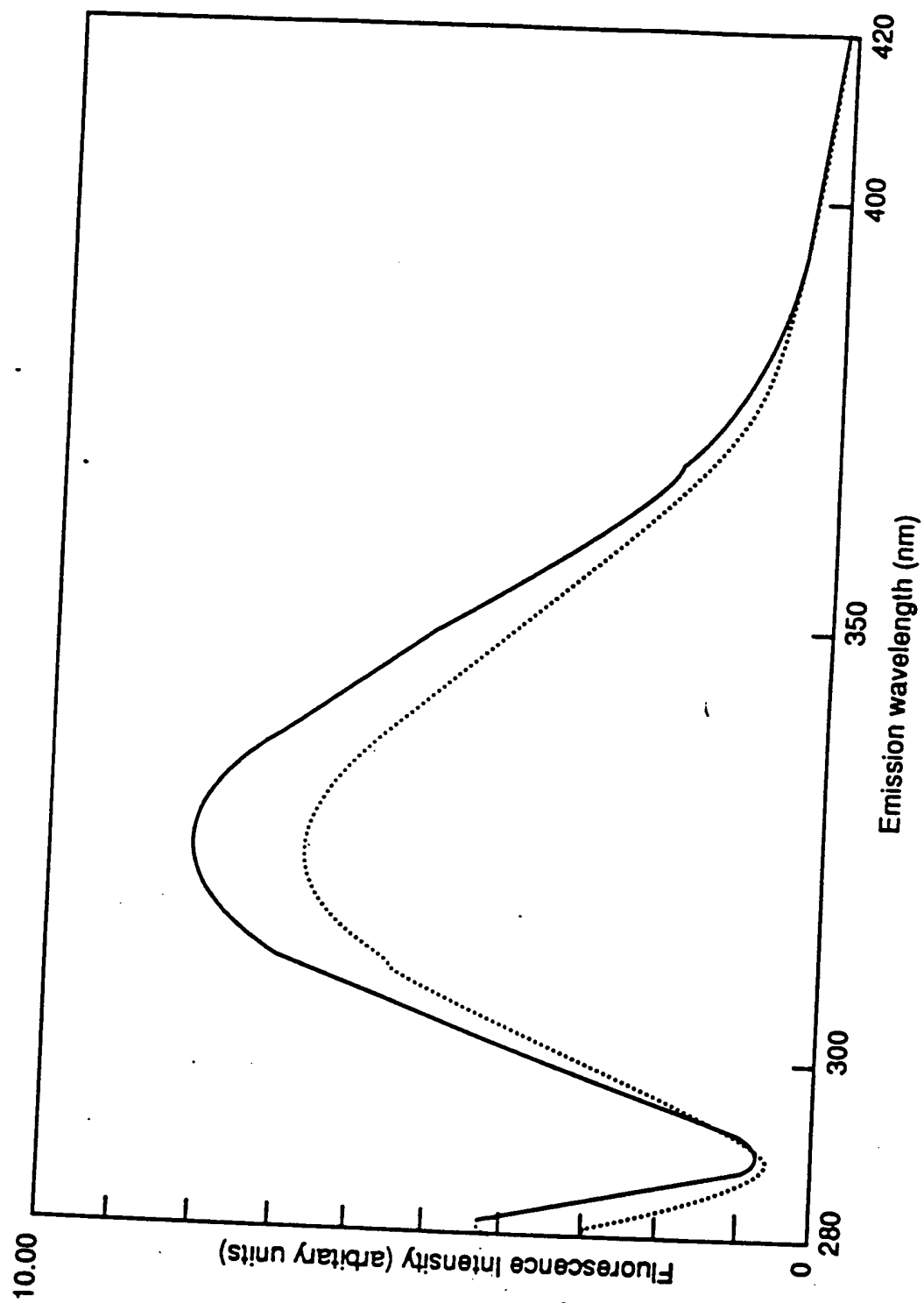


FIG. 69A

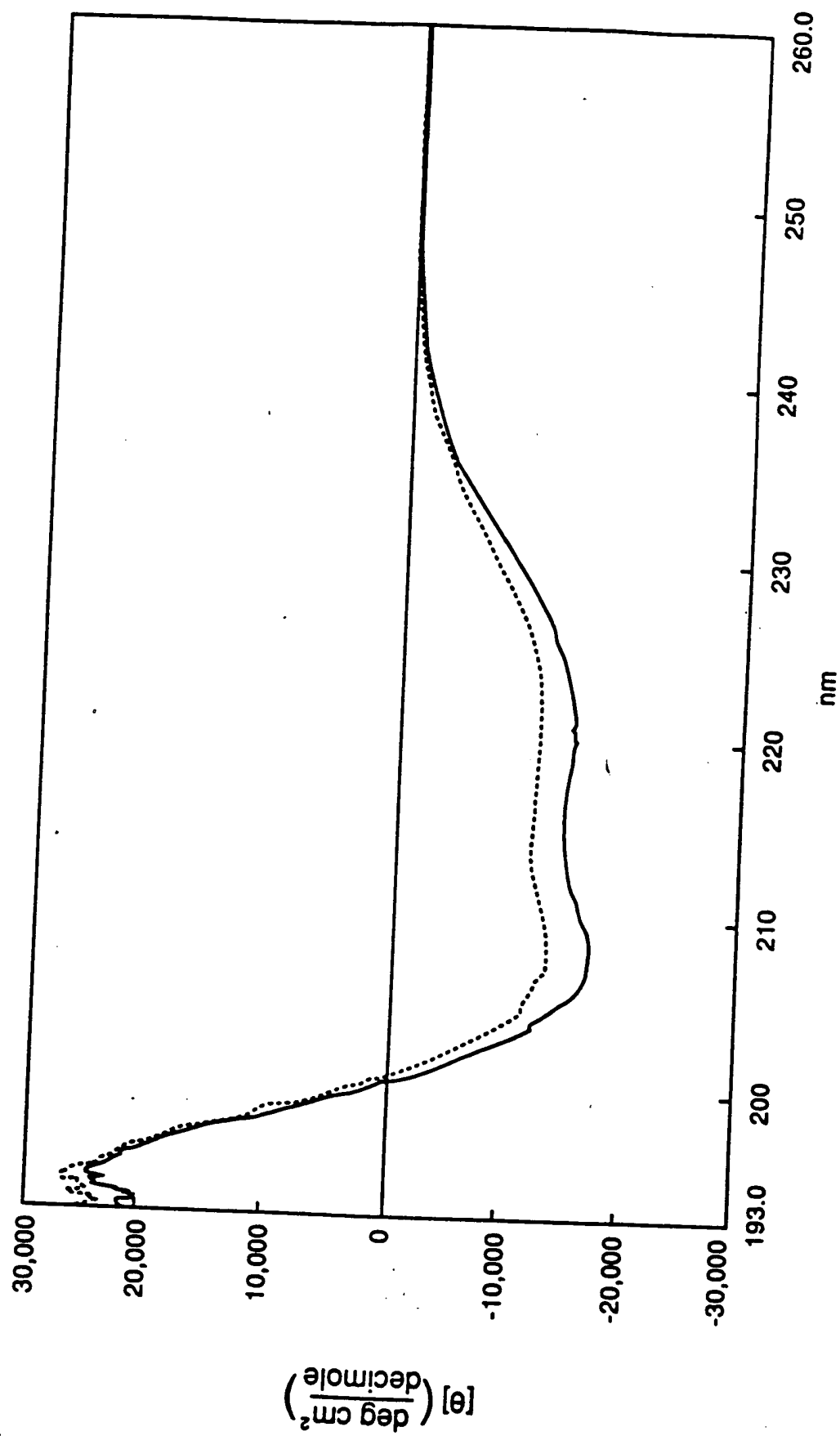


FIG. 69B

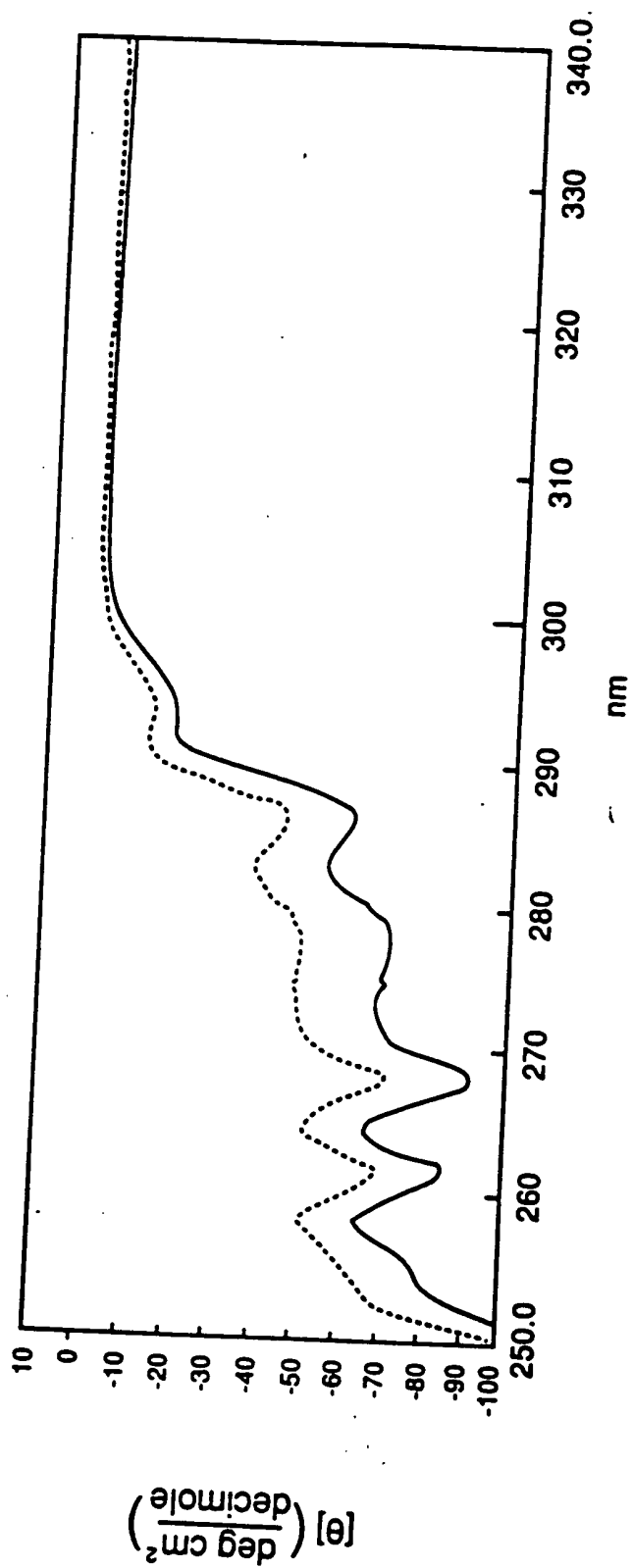


FIG. 70

